GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 20, 2004, 03:23:29 ; Search time 192 Seconds
(without alignments)
8373.982 Million cell updates/sec

Title: US-10-067-125-2
Perfect score: 2262
Sequence: 1 gaattccggcgcgctgcgac.....attaaaccattacaaatctc 2262

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 682300

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20.6	0.9	21	4	US-09-657-472-1764	Sequence 1764, Ap
2	c	20	0.9	20	3	US-09-167-109-47	Sequence 47, Appl
3	c	20	0.9	20	3	US-09-167-109-48	Sequence 48, Appl
4	c	20	0.9	20	3	US-09-167-109-49	Sequence 49, Appl
5	c	20	0.9	20	3	US-09-167-109-50	Sequence 50, Appl
6	c	20	0.9	20	3	US-09-167-109-51	Sequence 51, Appl
7	c	20	0.9	20	3	US-09-167-109-52	Sequence 52, Appl
8	c	20	0.9	20	3	US-09-167-109-53	Sequence 53, Appl
9	c	20	0.9	20	3	US-09-167-109-54	Sequence 54, Appl
10	c	20	0.9	20	3	US-09-167-109-55	Sequence 55, Appl
11	c	20	0.9	20	3	US-09-167-109-56	Sequence 56, Appl
12	c	20	0.9	20	3	US-09-167-109-57	Sequence 57, Appl
13	c	20	0.9	20	3	US-09-167-109-58	Sequence 58, Appl
14	c	20	0.9	20	3	US-09-167-109-59	Sequence 59, Appl
15	c	20	0.9	20	3	US-09-167-109-60	Sequence 60, Appl
16	c	20	0.9	20	3	US-09-167-109-61	Sequence 61, Appl
17	c	20	0.9	20	3	US-09-167-109-62	Sequence 62, Appl
18	c	20	0.9	20	3	US-09-167-109-63	Sequence 63, Appl
19	c	20	0.9	20	3	US-09-167-109-64	Sequence 64, Appl
20	c	20	0.9	20	3	US-09-167-109-65	Sequence 65, Appl
21	c	20	0.9	20	3	US-09-167-109-66	Sequence 66, Appl
22	c	20	0.9	20	3	US-09-167-109-67	Sequence 67, Appl
23	c	20	0.9	20	3	US-09-167-109-68	Sequence 68, Appl
24	c	20	0.9	28	3	US-08-959-381A-10	Sequence 10, Appl
25	c	19	0.8	30	4	US-09-786-256C-18	Sequence 18, Appl
26		17.6	0.8	24	4	US-09-480-718-19	Sequence 19, Appl
27	c	17.6	0.8	24	4	US-09-480-718-20	Sequence 20, Appl
28	c	17.6	0.8	24	4	US-09-933-313B-19	Sequence 19, Appl
29		17.6	0.8	26	1	US-08-453-104-3	Sequence 3, Appli
30		17.6	0.8	26	2	US-08-694-824-3	Sequence 3, Appli
31		17.4	0.8	27	1	US-08-696-770-6	Sequence 6, Appli
32		17.4	0.8	27	2	US-09-015-557-6	Sequence 6, Appli
33		17.4	0.8	27	4	US-09-254-180C-71	Sequence 71, Appl
34	c	17.4	0.8	27	4	US-09-254-180C-116	Sequence 116, App
35	c	17.4	0.8	28	1	US-08-393-985-27	Sequence 27, Appl
36		17.4	0.8	30	1	US-08-435-350-25	Sequence 25, Appl
37	c	17.2	0.8	27	3	US-09-056-226-10	Sequence 10, Appl
38	c	17.2	0.8	30	2	US-08-442-809A-42	Sequence 42, Appl
39	c	17	0.8	26	4	US-09-330-245A-7	Sequence 7, Appli
40		17	0.8	27	2	US-08-447-430A-21	Sequence 21, Appl
41	c	17	0.8	27	2	US-08-447-430A-22	Sequence 22, Appl
42		17	0.8	27	3	US-08-513-974B-75	Sequence 75, Appl
43		17	0.8	27	4	US-09-342-673-21	Sequence 21, Appl
44	c	17	0.8	27	4	US-09-342-673-22	Sequence 22, Appl
45		17	0.8	29	3	US-09-045-583-45	Sequence 45, Appl
46		17	0.8	29	4	US-09-534-185-45	Sequence 45, Appl
47	c	17	0.8	30	2	US-08-790-963-36	Sequence 36, Appl
48	c	17	0.8	30	3	US-09-371-774-36	Sequence 36, Appl
49	c	16.8	0.7	20	3	US-09-167-109-69	Sequence 69, Appl
50	c	16.8	0.7	21	3	US-09-301-978C-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-657-472-1764
; Sequence 1764, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1764
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-1764

Query Match 0.9%; Score 20.6; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 3e+04;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy        434 GCCGCTGCCCGCTCATGCTGA 454
              ||||||||||:||||||||||
Db          1 GCCGCTGCCCRCTCATGCTGA 21
```

RESULT 2
US-09-167-109-47/c
; Sequence 47, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsert, Lex M.

```
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 47
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-47

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCCGGCGCGCTGCGAC 20
              ||||||||||||||||||||
Db         20 GAATTCCGGCGCGCTGCGAC 1


RESULT 3
US-09-167-109-48/c
; Sequence 48, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 48
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-48

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CGGCGCGCTGCGACCGTTGG 26
              ||||||||||||||||||||
Db         20 CGGCGCGCTGCGACCGTTGG 1


RESULT 4
US-09-167-109-49/c
; Sequence 49, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 49
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-49

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 GGTCACAGCTCTCATGGCTG 61
              ||||||||||||||||||||
Db         20 GGTCACAGCTCTCATGGCTG 1


RESULT 5
US-09-167-109-50/c
; Sequence 50, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 50
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-50

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 CTCATGGCTGCAGCTAGCGT 71
              ||||||||||||||||||||
Db         20 CTCATGGCTGCAGCTAGCGT 1


RESULT 6
US-09-167-109-51/c
; Sequence 51, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 51
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-51

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        185 CCTTCCAGGCGCAGTGTGGC 204
              ||||||||||||||||||||
Db         20 CCTTCCAGGCGCAGTGTGGC 1
```

```
RESULT 7
US-09-167-109-52/c
; Sequence 52, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 52
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-52

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        348 GGAGGTGGAGAGCCTGCCGG 367
              ||||||||||||||||||||
Db         20 GGAGGTGGAGAGCCTGCCGG 1


RESULT 8
US-09-167-109-53/c
; Sequence 53, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 53
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-53

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        422 GCTGCCACGAAGGCCGCTGC 441
              ||||||||||||||||||||
Db         20 GCTGCCACGAAGGCCGCTGC 1


RESULT 9
US-09-167-109-54/c
; Sequence 54, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 54
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-54

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        576 CGTGAAGGCGCACCACGAGG 595
              ||||||||||||||||||||
Db         20 CGTGAAGGCGCACCACGAGG 1


RESULT 10
US-09-167-109-55/c
; Sequence 55, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 55
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-55

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        675 GACTTGTGGCAAGTGTCGAG 694
              ||||||||||||||||||||
Db         20 GACTTGTGGCAAGTGTCGAG 1


RESULT 11
US-09-167-109-56/c
; Sequence 56, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
```

US-09-167-109-56

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 751 CAGGAGCACGAGGTGCAGTG 770
||||||||||||||||||||
Db 20 CAGGAGCACGAGGTGCAGTG 1

RESULT 12
US-09-167-109-57/c
; Sequence 57, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/09/167,109
; CURRENT FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-167-109-57

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 848 GGTCAGAGCTCCTGCAGAGG 867
||||||||||||||||||||
Db 20 GGTCAGAGCTCCTGCAGAGG 1

RESULT 13
US-09-167-109-58/c
; Sequence 58, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/09/167,109
; CURRENT FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-167-109-58

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 962 GCAGCCGGCAGCACCGGCTG 981
||||||||||||||||||||
Db 20 GCAGCCGGCAGCACCGGCTG 1

RESULT 14
US-09-167-109-59/c
; Sequence 59, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/09/167,109
; CURRENT FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-167-109-59

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1240 CTGAACGGCGACGGCACCGG 1259
||||||||||||||||||||
Db 20 CTGAACGGCGACGGCACCGG 1

RESULT 15
US-09-167-109-60/c
; Sequence 60, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/09/167,109
; CURRENT FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-167-109-60

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1387 GACGCCTTCAGGCCCGACGT 1406
||||||||||||||||||||
Db 20 GACGCCTTCAGGCCCGACGT 1

RESULT 16
US-09-167-109-61/c
; Sequence 61, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321

```
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 61
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-61

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1533 GGCCATTGTGGACCTGACAG 1552
              ||||||||||||||||||||
Db         20 GGCCATTGTGGACCTGACAG 1


RESULT 17
US-09-167-109-62/c
; Sequence 62, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 62
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-62

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1590 GGCAGCCAGGCACAGCCGGC 1609
              ||||||||||||||||||||
Db         20 GGCAGCCAGGCACAGCCGGC 1


RESULT 18
US-09-167-109-63/c
; Sequence 63, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 63
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-63

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1685 GGTGTCGGCCTGCAGCCAAG 1704
              ||||||||||||||||||||
Db         20 GGTGTCGGCCTGCAGCCAAG 1


RESULT 19
US-09-167-109-64/c
; Sequence 64, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 64
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-64

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1789 GGCTGTGGTGGCATTGGCCG 1808
              ||||||||||||||||||||
Db         20 GGCTGTGGTGGCATTGGCCG 1


RESULT 20
US-09-167-109-65/c
; Sequence 65, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 65
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-65

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1916 CCATGTAGCAGGAGCACAGT 1935
              ||||||||||||||||||||
Db         20 CCATGTAGCAGGAGCACAGT 1


RESULT 21
US-09-167-109-66/c
```

```
; Sequence 66, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 66
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-66

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1994 GGCCTCCTGCTGGCCAGAGC 2013
             ||||||||||||||||||||
Db         20 GGCCTCCTGCTGGCCAGAGC 1


RESULT 22
US-09-167-109-67/c
; Sequence 67, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 67
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-67

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2117 CTTGGCCAGGCTGGCTGTGG 2136
             ||||||||||||||||||||
Db         20 CTTGGCCAGGCTGGCTGTGG 1


RESULT 23
US-09-167-109-68/c
; Sequence 68, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 68
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-09-167-109-68

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2221 TCCAGCTCACGAAGACAGAG 2240
             ||||||||||||||||||||
Db         20 TCCAGCTCACGAAGACAGAG 1


RESULT 24
US-08-959-381A-10/c
; Sequence 10, Application US/08959381A
; Patent No. 6048711
;  GENERAL INFORMATION:
;    APPLICANT:  HINUMA, SHUJI
;    APPLICANT:  FUKUSUMI, SHOJI
;    APPLICANT:  KAWAMATA, YUJI
;    TITLE OF INVENTION:  NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
;    TITLE OF INVENTION:  POLYNUCLEOTIDES
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ratner & Prestia
;      STREET:  P.O. Box 980
;      CITY:  Valley Forge
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,381A
;      FILING DATE:  28-OCT-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  286823/1996
;      FILING DATE:  29-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Prestia, Paul F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  TAK-50003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0700
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-959-381A-10

  Query Match             0.9%;  Score 20;  DB 3;  Length 28;
  Best Local Similarity   82.1%;  Pred. No. 4.8e+04;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        213 CTGCTCCTTCTGCCTGGCCAGCATCCTC 240
              ||||| |||||||||| ||| | || ||
Db         28 CTGCTACTTCTGCCTGCCCATCCTCTTC 1
```

```
RESULT 25
US-09-786-256C-18/c
; Sequence 18, Application US/09786256C
; Patent No. 6680189
; GENERAL INFORMATION:
;  APPLICANT: YOSHIMURA, Koji
;  APPLICANT:  HIKICHI, Yuichi
;  APPLICANT:  NISHIMURA, Atsushi
;  TITLE OF INVENTION: No. 6680189el Protein and DNA Thereof
;  FILE REFERENCE: 2544 US0P
;  CURRENT APPLICATION NUMBER: US/09/786,256C
;  CURRENT FILING DATE:  2001-03-02
;  PRIOR APPLICATION NUMBER: PCT/JP99/04766
;  PRIOR FILING DATE: 1999-09-02
;  PRIOR APPLICATION NUMBER: JP 10-250115
;  PRIOR FILING DATE: 1998-09-03
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Nucleic Acid Primer
US-09-786-256C-18

  Query Match             0.8%;  Score 19;  DB 4;  Length 30;
  Best Local Similarity   81.5%;  Pred. No. 8.8e+04;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        703 AGATTCCACGCCATCGGCTGCCTCGAG 729
              ||||||||| | ||  |||| |||||||
Db         27 AGATTCCAAGTCAATGGCTTCCTCGAG 1


RESULT 26
US-09-480-718-19
; Sequence 19, Application US/09480718
; Patent No. 6407062
; GENERAL INFORMATION:
;  APPLICANT: Sherr, Charles J
;  APPLICANT: Quelle, Dawn E
;  APPLICANT: Weber, Jason D.
;  APPLICANT: Roussel, Martine F.
;  APPLICANT: Frederique, Zindy
;  TITLE OF INVENTION: ARF-19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE
;  FILE REFERENCE: 1340-1-023 CIP 1
;  CURRENT APPLICATION NUMBER: US/09/480,718
;  CURRENT FILING DATE: 2000-01-07
;  EARLIER APPLICATION NUMBER: 09/129,855
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer(sense)
US-09-480-718-19

  Query Match             0.8%;  Score 17.6;  DB 4;  Length 24;
  Best Local Similarity   83.3%;  Pred. No. 1.8e+05;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1978 GCTGCTCCAGGAGAAGGGCCTCCT 2001
              ||||||||| | | ||||| ||||
Db          1 GCTGCTCCACGGGGAGGGCTTCCT 24


RESULT 27
US-09-480-718-20/c
; Sequence 20, Application US/09480718
; Patent No. 6407062
; GENERAL INFORMATION:
;  APPLICANT: Sherr, Charles J
;  APPLICANT: Quelle, Dawn E
;  APPLICANT: Weber, Jason D.
;  APPLICANT: Roussel, Martine F.
;  APPLICANT: Frederique, Zindy
;  TITLE OF INVENTION: ARF-19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE
;  FILE REFERENCE: 1340-1-023 CIP 1
;  CURRENT APPLICATION NUMBER: US/09/480,718
;  CURRENT FILING DATE: 2000-01-07
;  EARLIER APPLICATION NUMBER: 09/129,855
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Primer(antisense)
US-09-480-718-20

  Query Match             0.8%;  Score 17.6;  DB 4;  Length 24;
  Best Local Similarity   83.3%;  Pred. No. 1.8e+05;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1978 GCTGCTCCAGGAGAAGGGCCTCCT 2001
              ||||||||| | | ||||| ||||
Db         24 GCTGCTCCACGGGGAGGGCTTCCT 1


RESULT 28
US-09-933-313B-19/c
; Sequence 19, Application US/09933313B
; Patent No. 6514737
; GENERAL INFORMATION:
;  APPLICANT: Zhu, Zhenyu
;  APPLICANT:  Xu, Shuang-yong
;  TITLE OF INVENTION: Method For Cloning And Expression Of AsiSI Restriction
;  TITLE OF INVENTION:  Endonuclease And AsiSI Methylase In E. coli
;  FILE REFERENCE: NEB-189
;  CURRENT APPLICATION NUMBER: US/09/933,313B
;  CURRENT FILING DATE:  2001-08-20
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Arthrobacter sp.
US-09-933-313B-19

  Query Match             0.8%;  Score 17.6;  DB 4;  Length 24;
  Best Local Similarity   83.3%;  Pred. No. 1.8e+05;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1028 AGAGGAGCATTGGCCTCAAGGACC 1051
              ||| | || | ||||||||||||||
Db         24 AGAAGGGCGTCGGCCTCAAGGACC 1


RESULT 29
US-08-453-104-3
; Sequence 3, Application US/08453104
; Patent No. 5633446
;  GENERAL INFORMATION:
;    APPLICANT:  CORNELISSEN, Marc
;    APPLICANT:  SOETAERT, Piet
;    APPLICANT:  STAM, Maike
;    APPLICANT:  DOCKX, Jan
;    TITLE OF INVENTION:  MODIFIED BACILLUS THURINGIENSIS
```

```
;    TITLE OF INVENTION:  INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
;    TITLE OF INVENTION:  IN PLANT CELLS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  George Mason Bldg., Washington & Prince Sts.
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/453,104
;      FILING DATE:
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/937,869
;      FILING DATE:  16-DEC-1992
;      APPLICATION NUMBER:  GB 90401055.0
;      FILING DATE:  18-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rea, Teresa S
;      REGISTRATION NUMBER:  30,427
;      REFERENCE/DOCKET NUMBER:  010830-032
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-453-104-3

  Query Match             0.8%;  Score 17.6;  DB 1;  Length 26;
  Best Local Similarity   66.7%;  Pred. No. 1.9e+05;
  Matches   16;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1688 GTCGGCCTGCAGCCAAGTTCACTG 1711
                 |:|| ||:|||||||||  :  |:|
Db          2 GUCGACCUGCAGCCAAGCUUGCUG 25


RESULT 30
US-08-694-824-3
; Sequence 3, Application US/08694824
; Patent No. 5877306
;  GENERAL INFORMATION:
;    APPLICANT:  CORNELISSEN, Marc
;    APPLICANT:  SOETAERT, Piet
;    APPLICANT:  STAM, Maike
;    APPLICANT:  DOCKX, Jan
;    TITLE OF INVENTION:  MODIFIED BACILLUS THURINGIENSIS
;    TITLE OF INVENTION:  INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
;    TITLE OF INVENTION:  IN PLANT CELLS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  George Mason Bldg., Washington & Prince Sts.
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/694,824
;      FILING DATE:  09-AUG-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/937,869
;      FILING DATE:  16-DEC-1992
;      APPLICATION NUMBER:  GB 90401055.0
;      FILING DATE:  18-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rea, Teresa S
;      REGISTRATION NUMBER:  30,427
;      REFERENCE/DOCKET NUMBER:  010830-032
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-694-824-3

  Query Match             0.8%;  Score 17.6;  DB 2;  Length 26;
  Best Local Similarity   66.7%;  Pred. No. 1.9e+05;
  Matches   16;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1688 GTCGGCCTGCAGCCAAGTTCACTG 1711
                 |:|| ||:|||||||||  :  |:|
Db          2 GUCGACCUGCAGCCAAGCUUGCUG 25


RESULT 31
US-08-696-770-6
; Sequence 6, Application US/08696770
; Patent No. 5763218
;  GENERAL INFORMATION:
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Li, Yi
;    APPLICANT:  Ruben, Steven
;    APPLICANT:  Soppet, Daniel
;    TITLE OF INVENTION:  NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  709 Swedeland Road
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406-2799
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/696,770
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Han, William T
;      REGISTRATION NUMBER:  34,344
;      REFERENCE/DOCKET NUMBER:  TAK50001-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5219
;      TELEFAX:  610-270-5090
```

```
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
US-08-696-770-6

  Query Match             0.8%;  Score 17.4;  DB 1;  Length 27;
  Best Local Similarity   77.8%;  Pred. No. 2.1e+05;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1522 ATCTTCATCAAGGCCATTGTGGACCTG 1548
              ||| ||| || |||||| | ||| |||
Db          1 ATCCTCAACATGGCCATCGCGGAACTG 27


RESULT 32
US-09-015-557-6
; Sequence 6, Application US/09015557
; Patent No. 5932702
;  GENERAL INFORMATION:
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Li, Yi
;    APPLICANT:  Ruben, Steven
;    APPLICANT:  Soppet, Daniel
;    TITLE OF INVENTION:  NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  709 Swedeland Road
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406-2799
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/015,557
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/696,770
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Han, William T
;      REGISTRATION NUMBER:  34,344
;      REFERENCE/DOCKET NUMBER:  TAK50001-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5219
;      TELEFAX:  610-270-5090
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
US-09-015-557-6

  Query Match             0.8%;  Score 17.4;  DB 2;  Length 27;
  Best Local Similarity   77.8%;  Pred. No. 2.1e+05;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1522 ATCTTCATCAAGGCCATTGTGGACCTG 1548
              ||| ||| || |||||| | ||| |||
Db          1 ATCCTCAACATGGCCATCGCGGAACTG 27


RESULT 33
US-09-254-180C-71
; Sequence 71, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
;  APPLICANT: OKUMURA, Ko
;  APPLICANT:  EDA, Yasuyuki
;  APPLICANT:  MAEDA, Hiroaki
;  APPLICANT:  USHIO, Yoshitaka
;  APPLICANT:  HIGUCHI, Hirofumi
;  APPLICANT:  NAKATA, Motomi
;  TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
;  TITLE OF INVENTION:  Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
;  FILE REFERENCE: 050006-0055
;  CURRENT APPLICATION NUMBER: US/09/254,180C
;  CURRENT FILING DATE:  1999-04-15
;  PRIOR APPLICATION NUMBER: PCT/JP97/02983
;  PRIOR FILING DATE: 1997-08-27
;  PRIOR APPLICATION NUMBER: 271546/1996
;  PRIOR FILING DATE: 1996-09-20
;  PRIOR APPLICATION NUMBER: 231472/1996
;  PRIOR FILING DATE: 1996-09-02
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
;   LENGTH: 27
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: DNA Primer
US-09-254-180C-71

  Query Match             0.8%;  Score 17.4;  DB 4;  Length 27;
  Best Local Similarity   77.8%;  Pred. No. 2.1e+05;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1179 CATCTTCTCCCCAGCCTTCTACACCAG 1205
              |||| ||| ||| ||| ||  ||||||
Db          1 CATCATCTTCCCCGCCATCATCACCAG 27


RESULT 34
US-09-254-180C-116/c
; Sequence 116, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
;  APPLICANT: OKUMURA, Ko
;  APPLICANT:  EDA, Yasuyuki
;  APPLICANT:  MAEDA, Hiroaki
;  APPLICANT:  USHIO, Yoshitaka
;  APPLICANT:  HIGUCHI, Hirofumi
;  APPLICANT:  NAKATA, Motomi
;  TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
;  TITLE OF INVENTION:  Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
;  FILE REFERENCE: 050006-0055
;  CURRENT APPLICATION NUMBER: US/09/254,180C
;  CURRENT FILING DATE:  1999-04-15
;  PRIOR APPLICATION NUMBER: PCT/JP97/02983
;  PRIOR FILING DATE: 1997-08-27
;  PRIOR APPLICATION NUMBER: 271546/1996
;  PRIOR FILING DATE: 1996-09-20
;  PRIOR APPLICATION NUMBER: 231472/1996
```

```
;  PRIOR FILING DATE: 1996-09-02
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 116
;   LENGTH: 27
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: DNA Primer
US-09-254-180C-116

  Query Match             0.8%;  Score 17.4;  DB 4;  Length 27;
  Best Local Similarity   77.8%;  Pred. No. 2.1e+05;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1179 CATCTTCTCCCCAGCCTTCTACACCAG 1205
              |||| ||| ||| ||| ||  ||||||
Db         27 CATCATCTTCCCCGCCATCATCACCAG 1


RESULT 35
US-08-393-985-27/c
; Sequence 27, Application US/08393985
; Patent No. 5693476
;  GENERAL INFORMATION:
;    APPLICANT:  Scheller, Richard H.
;    TITLE OF INVENTION:  Methods and Compositions for Modulation
;    TITLE OF INVENTION:  of Vesicular Release
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/393,985
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sholtz, Charles K.
;      REGISTRATION NUMBER:  38,615
;      REFERENCE/DOCKET NUMBER:  8600-0152
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  oligonucleotide used for mutant M4
US-08-393-985-27

  Query Match             0.8%;  Score 17.4;  DB 1;  Length 28;
  Best Local Similarity   77.8%;  Pred. No. 2.2e+05;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1180 ATCTTCTCCCCAGCCTTCTACACCAGC 1206
              ||| ||||||| ||  ||| | |||||
Db         27 ATCATCTCCCCCGCGCTCTCCGCCAGC 1


RESULT 36
US-08-435-350-25
; Sequence 25, Application US/08435350
; Patent No. 5599704
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  TREATMENT OF BREAST CANCER
;    NUMBER OF SEQUENCES:  118
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,350
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936,531
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  197/245
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-350-25

  Query Match             0.8%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   59.3%;  Pred. No. 2.2e+05;
  Matches   16;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1458 CTGCCCCCTCTTCTGCCCCGTCTCCAA 1484
              |:|| |||:| :|:||||| :   |||
Db          2 CUGCACCCUCGUCUGCCCCCUGCACAA 28


RESULT 37
US-09-056-226-10/c
; Sequence 10, Application US/09056226B
; Patent No. 6177614
; GENERAL INFORMATION:
;  APPLICANT: Colasanti, Joseph J.
;  APPLICANT: Sundaresan, Venkatesan
;  TITLE OF INVENTION: Control of Floral Induction in Plants
;  TITLE OF INVENTION: and Uses Therefor
;  FILE REFERENCE: CSHL94-04A4
;  CURRENT APPLICATION NUMBER: US/09/056,226B
;  CURRENT FILING DATE: 1998-04-07
;  EARLIER APPLICATION NUMBER: US 09/000,640
;  EARLIER FILING DATE: 1997-12-30
;  EARLIER APPLICATION NUMBER: US 08/804,104
;  EARLIER FILING DATE: 1997-02-20
;  EARLIER APPLICATION NUMBER: PCT/US96/03466
;  EARLIER FILING DATE: 1996-03-15
```

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;  EARLIER APPLICATION NUMBER: US 08/406,186
;  EARLIER FILING DATE: 1995-03-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 27
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (19)...(19)
;   OTHER INFORMATION: 'N' at position 19 represents the insertion site
;   OTHER INFORMATION: of the DS2 transposon.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(27)
;   OTHER INFORMATION: n = A,T,C or G
US-09-056-226-10

  Query Match             0.8%;  Score 17.2;  DB 3;  Length 27;
  Best Local Similarity   82.6%;  Pred. No. 2.4e+05;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        871 GAGAGCCTGGAGAAGAAGACGGC 893
              |||| |||||||||||  || | |
Db         23 GAGANCCTGGAGAAGAGGATGCC 1


RESULT 38
US-08-442-809A-42/c
; Sequence 42, Application US/08442809A
; Patent No. 5976873
;  GENERAL INFORMATION:
;    APPLICANT:  Bohinski, Robert J.,
;    APPLICANT:  Whitsett, Jeffrey A.
;    TITLE OF INVENTION:  Nucleic Acid Sequences
;    TITLE OF INVENTION:  Controlling Lung Cell -
;    TITLE OF INVENTION:  Specific Gene Expression
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,809A
;      FILING DATE:  17-MAY-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/245,356
;      FILING DATE:  18-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  271010-360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
US-08-442-809A-42

  Query Match             0.8%;  Score 17.2;  DB 2;  Length 30;
  Best Local Similarity   73.3%;  Pred. No. 2.5e+05;
  Matches   22;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        847 GGGTCAGAGCTCCTGCAGAGGTGCGAGAGC 876
              | |||| | || |||||| ||  |||| ||
Db         30 GAGTCACACCTGCTGCAGTGGCTCGAGCGC 1


RESULT 39
US-09-330-245A-7/c
; Sequence 7, Application US/09330245A
; Patent No. 6432631
; GENERAL INFORMATION:
;  APPLICANT:  GILEAD SCIENCES, INC. et al.
;  TITLE OF INVENTION:  NOVEL GENE ENCODING ORGANIC ANION TRANSPORTER
;  FILE REFERENCE:  240.1PCnew
;  CURRENT APPLICATION NUMBER: US/09/330,245A
;  CURRENT FILING DATE:  1999-06-10
;  PRIOR APPLICATION NUMBER:  60/088,864
;  PRIOR FILING DATE:  1998-06-11
;  PRIOR APPLICATION NUMBER:  60/132,267
;  PRIOR FILING DATE:  1999-05-03
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 26
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:This information
;   OTHER INFORMATION: is not available.
US-09-330-245A-7

  Query Match             0.8%;  Score 17;  DB 4;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+05;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        939 GGTGGCCATGACTGCCGAGGCCTGC 963
              ||||  ||||||||||||||  || |
Db         25 GGTGAGCATGACTGCCGAGCTCTAC 1


RESULT 40
US-08-447-430A-21
; Sequence 21, Application US/08447430A
; Patent No. 5916558
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Recombinant polypeptides and peptides,
;    TITLE OF INVENTION:  nucleic acids coding for the same and use of these
;    TITLE OF INVENTION:  polypeptides and peptides in the diagnostic of
;    TITLE OF INVENTION:  tuberculosis.
;    NUMBER OF SEQUENCES:  43
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,430A
;      FILING DATE:
;      CLASSIFICATION:  424
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
```

```
;    ANTI-SENSE:  NO
US-08-447-430A-21

  Query Match             0.8%;  Score 17;  DB 2;  Length 27;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+05;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1041 CCTCAAGGACCTGGCGATGGCTGAC 1065
              ||| |  | ||||||||||| ||||
Db          1 CCTGATCGGCCTGGCGATGGGTGAC 25


RESULT 41
US-08-447-430A-22/c
; Sequence 22, Application US/08447430A
; Patent No. 5916558
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Recombinant polypeptides and peptides,
;    TITLE OF INVENTION:  nucleic acids coding for the same and use of these
;    TITLE OF INVENTION:  polypeptides and peptides in the diagnostic of
;    TITLE OF INVENTION:  tuberculosis.
;    NUMBER OF SEQUENCES:  43
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,430A
;      FILING DATE:
;      CLASSIFICATION:  424
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-447-430A-22

  Query Match             0.8%;  Score 17;  DB 2;  Length 27;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+05;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1041 CCTCAAGGACCTGGCGATGGCTGAC 1065
              ||| |  | ||||||||||| ||||
Db         27 CCTGATCGGCCTGGCGATGGGTGAC 3


RESULT 42
US-08-513-974B-75
; Sequence 75, Application US/08513974B
; Patent No. 6114139
;  GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Ohtaki, Tetsuya
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Ohgi, Kazuhiro
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;    TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;    NUMBER OF SEQUENCES:  380
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/513,974B
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP95/01599
;      FILING DATE:  10-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-093989
;      FILING DATE:  19-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-057186
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-007177
;      FILING DATE:  20-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-326611
;      FILING DATE:  28-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-270017
;      FILING DATE:  02-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-236357
;      FILING DATE:  30-SEP-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-236356
;      FILING DATE:  30-SEP-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189274
;      FILING DATE:  11-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189273
;      FILING DATE:  11-AUG-1945
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189272
;      FILING DATE:  11-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Resnick, David S.
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  45753
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-513-974B-75

  Query Match             0.8%;  Score 17;  DB 3;  Length 27;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+05;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        542 GCCGGCATTGCCGGGCACCCTGCTG 566
              || |||| || |||||| | |||||
Db          1 GCTGGCAGTGGCGGGCAACGTGCTG 25


RESULT 43
US-09-342-673-21
; Sequence 21, Application US/09342673
; Patent No. 6531138
;  GENERAL INFORMATION:
;    APPLICANT:
```

```
;    TITLE OF INVENTION:  Recombinant polypeptides and peptides,
;    TITLE OF INVENTION:  nucleic acids coding for the same and use of these
;    TITLE OF INVENTION:  polypeptides and peptides in the diagnostic of
;    TITLE OF INVENTION:  tuberculosis.
;    NUMBER OF SEQUENCES:  43
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/342,673
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/447,430
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-342-673-21

  Query Match             0.8%;  Score 17;  DB 4;  Length 27;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+05;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1041 CCTCAAGGACCTGGCGATGGCTGAC 1065
             ||| |  | ||||||||||| ||||
Db          1 CCTGATCGGCCTGGCGATGGGTGAC 25


RESULT 44
US-09-342-673-22/c
; Sequence 22, Application US/09342673
; Patent No. 6531138
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Recombinant polypeptides and peptides,
;    TITLE OF INVENTION:  nucleic acids coding for the same and use of these
;    TITLE OF INVENTION:  polypeptides and peptides in the diagnostic of
;    TITLE OF INVENTION:  tuberculosis.
;    NUMBER OF SEQUENCES:  43
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/342,673
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/447,430
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-342-673-22

  Query Match             0.8%;  Score 17;  DB 4;  Length 27;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+05;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1041 CCTCAAGGACCTGGCGATGGCTGAC 1065
             ||| |  | ||||||||||| ||||
Db         27 CCTGATCGGCCTGGCGATGGGTGAC 3


RESULT 45
US-09-045-583-45
; Sequence 45, Application US/09045583
; Patent No. 6287805
;  GENERAL INFORMATION:
;    APPLICANT:  Graham, Gerard J. et al.
;    TITLE OF INVENTION:  No. 6287805el Molecules of the G Protein-Coupled
;    NUMBER OF SEQUENCES:  56
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/045,583
;      FILING DATE:  20-MAR-98
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  MNI-044
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  45:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  29 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-045-583-45

  Query Match             0.8%;  Score 17;  DB 3;  Length 29;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+05;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1040 GCCTCAAGGACCTGGCGATGGCTGA 1064
             |||||| | |||||||||| | | |
Db          3 GCCTCAGGTACCTGGCGATCGTTCA 27


RESULT 46
US-09-534-185-45
; Sequence 45, Application US/09534185
; Patent No. 6403767
;   GENERAL INFORMATION:
;        APPLICANT: Graham, Gerard J. et al.
;        TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
;                            Heptahelical Receptor Superfamily and Uses
;                            Therefor
;        NUMBER OF SEQUENCES: 56
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: LAHIVE & COCKFIELD, LLP
;             STREET: 28 State Street
;             CITY: Boston
```

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;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02109
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/534,185
;             FILING DATE: 24-Mar-2000
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/045,583
;             FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Mandragouras, Amy E.
;             REGISTRATION NUMBER: 36,207
;             REFERENCE/DOCKET NUMBER: MNI-044
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617)227-7400
;             TELEFAX: (617)742-4214
;   INFORMATION FOR SEQ ID NO: 45:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 29 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-534-185-45

  Query Match             0.8%;  Score 17;  DB 4;  Length 29;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+05;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1040 GCCTCAAGGACCTGGCGATGGCTGA 1064
             |||||| | |||||||||| | | |
Db          3 GCCTCAGGTACCTGGCGATCGTTCA 27


RESULT 47
US-08-790-963-36/c
; Sequence 36, Application US/08790963
; Patent No. 5837464
;  GENERAL INFORMATION:
;    APPLICANT:  Daniel J. Capon
;    APPLICANT:  Christos John Petropoulous
;    TITLE OF INVENTION:  Compositions And Methods For
;    TITLE OF INVENTION:  Determining Anti-viral Drug Susceptibility And
;    TITLE OF INVENTION:  Resistance
;    NUMBER OF SEQUENCES:  105
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patentin Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/790,963
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  50130-B/JPW/AKC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0526
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-790-963-36

  Query Match             0.8%;  Score 17;  DB 2;  Length 30;
  Best Local Similarity   80.0%;  Pred. No. 2.8e+05;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         51 TCTCATGGCTGCAGCTAGCGTGACC 75
              | ||||| ||| |||||||||| | |
Db         25 TATCATGTCTGGAGCTAGCGTTAAC 1


RESULT 48
US-09-371-774-36/c
; Sequence 36, Application US/09371774
; Patent No. 6242187
;  GENERAL INFORMATION:
;       APPLICANT: Daniel J. Capon
;                  Christos John Petropoulous
;       TITLE OF INVENTION: Compositions And Methods For
;                           Determining Anti-viral Drug Susceptibility And
;                           Resistance and Anti-viral Drug Screening
;       NUMBER OF SEQUENCES: 105
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Cooper & Dunham LLP
;            STREET: 1185 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: United States
;            ZIP: 10036
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: Patentin Release #1.0, Version#1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/371,774
;            FILING DATE: 10-Aug-1999
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: White, John P.
;            REGISTRATION NUMBER: 28,678
;            REFERENCE/DOCKET NUMBER: 50130-F/JPW/CMR
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 212-278-0400
;            TELEFAX: 212-391-0526
;   INFORMATION FOR SEQ ID NO: 36:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 30 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-371-774-36

  Query Match             0.8%;  Score 17;  DB 3;  Length 30;
  Best Local Similarity   80.0%;  Pred. No. 2.8e+05;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         51 TCTCATGGCTGCAGCTAGCGTGACC 75
              | ||||| ||| |||||||||| | |
Db         25 TATCATGTCTGGAGCTAGCGTTAAC 1
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RESULT 49
US-09-167-109-69/c
; Sequence 69, Application US/09167109
; Patent No. 6399297
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT: Monia, Brett P.
;  APPLICANT: Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/09/167,109
;  CURRENT FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 69
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: control sequence
US-09-167-109-69

  Query Match             0.7%;  Score 16.8;  DB 3;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 2.7e+05;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        576 CGTGAAGGCGCACCACGAGG 595
              ||||||| |||| |||||||
Db         20 CGTGAAGCCGCAGCACGAGG 1


RESULT 50
US-09-301-978C-7/c
; Sequence 7, Application US/09301978C
; Patent No. 6392015
; GENERAL INFORMATION:
;  APPLICANT: Panganiban, Antonito
;  APPLICANT:  Callahan, Mark A.
;  TITLE OF INVENTION: Method of Identifying Modulators of HIV-1 VPU and GAG
;  TITLE OF INVENTION:  Interaction with U Binding Protein (UBP)
;  FILE REFERENCE: 960296.95335
;  CURRENT APPLICATION NUMBER: US/09/301,978C
;  CURRENT FILING DATE:  1999-04-29
;  PRIOR APPLICATION NUMBER: 60/083,567
;  PRIOR FILING DATE: 1998-04-30
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
;   OTHER INFORMATION: Primer
US-09-301-978C-7

  Query Match             0.7%;  Score 16.8;  DB 3;  Length 21;
  Best Local Similarity   90.0%;  Pred. No. 2.7e+05;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2030 CTTGGTTCTCCCCTCTGGCC 2049
              |||||||||| | |||||||
Db         20 CTTGGTTCTCTCATCTGGCC 1


Search completed: November 20, 2004, 09:22:31
Job time : 193 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 20, 2004, 04:29:03 ; Search time 1125 Seconds
(without alignments)
10864.885 Million cell updates/sec

Title: US-10-067-125-2
Perfect score: 2262
Sequence: 1 gaattccggcgcgctgcgac.....attaaaccattacaaatctc 2262

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 1535986

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Published_Applications_NA:*
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	24	1.1	24	16	US-10-409-107A-16	Sequence 16, Appl
	2	22.6	1.0	30	17	US-10-694-520-7	Sequence 7, Appli
	3	22	1.0	22	16	US-10-409-107A-15	Sequence 15, Appl
c	4	20	0.9	20	14	US-10-067-125-47	Sequence 47, Appl
c	5	20	0.9	20	14	US-10-067-125-48	Sequence 48, Appl
c	6	20	0.9	20	14	US-10-067-125-49	Sequence 49, Appl
c	7	20	0.9	20	14	US-10-067-125-50	Sequence 50, Appl
c	8	20	0.9	20	14	US-10-067-125-51	Sequence 51, Appl
c	9	20	0.9	20	14	US-10-067-125-52	Sequence 52, Appl
c	10	20	0.9	20	14	US-10-067-125-53	Sequence 53, Appl
c	11	20	0.9	20	14	US-10-067-125-54	Sequence 54, Appl
c	12	20	0.9	20	14	US-10-067-125-55	Sequence 55, Appl
c	13	20	0.9	20	14	US-10-067-125-56	Sequence 56, Appl
c	14	20	0.9	20	14	US-10-067-125-57	Sequence 57, Appl
c	15	20	0.9	20	14	US-10-067-125-58	Sequence 58, Appl
c	16	20	0.9	20	14	US-10-067-125-59	Sequence 59, Appl
c	17	20	0.9	20	14	US-10-067-125-60	Sequence 60, Appl
c	18	20	0.9	20	14	US-10-067-125-61	Sequence 61, Appl
c	19	20	0.9	20	14	US-10-067-125-62	Sequence 62, Appl
c	20	20	0.9	20	14	US-10-067-125-63	Sequence 63, Appl
c	21	20	0.9	20	14	US-10-067-125-64	Sequence 64, Appl
c	22	20	0.9	20	14	US-10-067-125-65	Sequence 65, Appl
c	23	20	0.9	20	14	US-10-067-125-66	Sequence 66, Appl
c	24	20	0.9	20	14	US-10-067-125-67	Sequence 67, Appl
c	25	20	0.9	20	14	US-10-067-125-68	Sequence 68, Appl
c	26	19	0.8	30	17	US-10-726-148A-18	Sequence 18, Appl
c	27	18.6	0.8	29	9	US-09-950-335A-4	Sequence 4, Appli
	28	18.6	0.8	30	16	US-10-380-584-67	Sequence 67, Appl
	29	18.4	0.8	25	15	US-10-098-263B-67634	Sequence 67634, A
	30	18.4	0.8	30	13	US-10-081-281-18	Sequence 18, Appl
c	31	18.2	0.8	25	15	US-10-098-263B-42324	Sequence 42324, A
	32	17.8	0.8	29	9	US-09-879-813-7	Sequence 7, Appli
	33	17.8	0.8	29	10	US-09-828-717-7	Sequence 7, Appli
	34	17.8	0.8	29	15	US-10-146-505-7	Sequence 7, Appli
	35	17.8	0.8	30	14	US-10-157-382-4	Sequence 4, Appli
c	36	17.6	0.8	25	15	US-10-098-263B-48292	Sequence 48292, A
c	37	17.6	0.8	25	15	US-10-098-263B-130463	Sequence 130463,
c	38	17.6	0.8	25	15	US-10-098-263B-130464	Sequence 130464,
	39	17.4	0.8	29	16	US-10-262-839-342	Sequence 342, App
	40	17.4	0.8	30	13	US-10-081-281-22	Sequence 22, Appl
	41	17.4	0.8	30	16	US-10-343-810-12	Sequence 12, Appl
	42	17.2	0.8	23	15	US-10-244-647-1317	Sequence 1317, Ap
c	43	17.2	0.8	25	15	US-10-098-263B-80858	Sequence 80858, A
	44	17.2	0.8	25	17	US-10-717-597-2427	Sequence 2427, Ap
c	45	17.2	0.8	30	9	US-09-320-337-42	Sequence 42, Appl
	46	17	0.8	25	14	US-10-215-112-4521	Sequence 4521, Ap
	47	17	0.8	25	15	US-10-098-263B-8292	Sequence 8292, Ap
c	48	17	0.8	25	15	US-10-098-263B-32545	Sequence 32545, A
c	49	17	0.8	25	15	US-10-098-263B-50938	Sequence 50938, A
c	50	17	0.8	25	15	US-10-098-263B-54431	Sequence 54431, A

ALIGNMENTS

RESULT 1
US-10-409-107A-16/c
; Sequence 16, Application US/10409107A
; Publication No. US20040053288A1
; GENERAL INFORMATION:
; APPLICANT: YANAI, Yoshiaki
; APPLICANT: YAMAMOTO, Shigeto
; APPLICANT: YAMAMOTO, Kozo
; APPLICANT: IKEGAMI, Hakuo
; TITLE OF INVENTION: Method for estimating therapeutic efficacy of tumor necrosis
; TITLE OF INVENTION: factor
; FILE REFERENCE: YANAI=3
; CURRENT APPLICATION NUMBER: US/10/409,107A
; CURRENT FILING DATE: 2003-04-19
; PRIOR APPLICATION NUMBER: JP 107126/2002
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide used as primer for PCR detection of TRAF2 mRNA
US-10-409-107A-16

Query Match 1.1%; Score 24; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1223 TGTGTCTGCGTATCTACCTGAACG 1246
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Db         24 TGTGTCTGCGTATCTACCTGAACG 1
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RESULT 2
US-10-694-520-7
; Sequence 7, Application US/10694520
; Publication No. US20040170614A1
; GENERAL INFORMATION:
; APPLICANT: University of Iowa Research Foundation
; APPLICANT: Bishop, G.
; APPLICANT: Hostager, B. S.
; TITLE OF INVENTION: Somatic cell gene targeting vectors and methods of use thereof
; FILE REFERENCE: 875.061US1
; CURRENT APPLICATION NUMBER: US/10/694,520
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: US 60/422,674
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic primer.
US-10-694-520-7

Query Match 1.0%; Score 22.6; DB 17; Length 30;
Best Local Similarity 86.2%; Pred. No. 3e+04;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy        244 TCTGGGCCTCAGAACTGTGCTGCCTGTGT 272
              | |||  | ||||||||||||||||||||||
Db          1 TTTGGTACCCAGAACTGTGCTGCCTGTGT 29
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RESULT 3
US-10-409-107A-15
; Sequence 15, Application US/10409107A
; Publication No. US20040053288A1
; GENERAL INFORMATION:
; APPLICANT: YANAI, Yoshiaki
; APPLICANT: YAMAMOTO, Shigeto
; APPLICANT: YAMAMOTO, Kozo
; APPLICANT: IKEGAMI, Hakuo
; TITLE OF INVENTION: Method for estimating therapeutic efficacy of tumor necrosis
; TITLE OF INVENTION: factor
; FILE REFERENCE: YANAI=3
; CURRENT APPLICATION NUMBER: US/10/409,107A
; CURRENT FILING DATE: 2003-04-19
; PRIOR APPLICATION NUMBER: JP 107126/2002
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide used as primer for PCR detection of TRAF2 mRNA
US-10-409-107A-15

Query Match 1.0%; Score 22; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        904 AACATTGTCTGCGTCCTGAACC 925
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Db          1 AACATTGTCTGCGTCCTGAACC 22
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RESULT 4
US-10-067-125-47/c
; Sequence 47, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/10/067,125
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/167,109
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-067-125-47

Query Match 0.9%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAATTCCGGCGCGCTGCGAC 20
              ||||||||||||||||||||
Db         20 GAATTCCGGCGCGCTGCGAC 1
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RESULT 5
US-10-067-125-48/c
; Sequence 48, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/10/067,125
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/167,109
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-067-125-48

Query Match 0.9%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          7 CGGCGCGCTGCGACCGTTGG 26
              ||||||||||||||||||||
Db         20 CGGCGCGCTGCGACCGTTGG 1
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RESULT 6
US-10-067-125-49/c
; Sequence 49, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsert, Lex M.

```
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 49
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-49

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 GGTCACAGCTCTCATGGCTG 61
              ||||||||||||||||||||
Db         20 GGTCACAGCTCTCATGGCTG 1


RESULT 7
US-10-067-125-50/c
; Sequence 50, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 50
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-50

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 CTCATGGCTGCAGCTAGCGT 71
              ||||||||||||||||||||
Db         20 CTCATGGCTGCAGCTAGCGT 1


RESULT 8
US-10-067-125-51/c
; Sequence 51, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 51
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-51

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        185 CCTTCCAGGCGCAGTGTGGC 204
              ||||||||||||||||||||
Db         20 CCTTCCAGGCGCAGTGTGGC 1


RESULT 9
US-10-067-125-52/c
; Sequence 52, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 52
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-52

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        348 GGAGGTGGAGAGCCTGCCGG 367
              ||||||||||||||||||||
Db         20 GGAGGTGGAGAGCCTGCCGG 1


RESULT 10
US-10-067-125-53/c
; Sequence 53, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 53
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

```
;   OTHER INFORMATION: antisense sequence
US-10-067-125-53

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        422 GCTGCCACGAAGGCCGCTGC 441
              ||||||||||||||||||||
Db         20 GCTGCCACGAAGGCCGCTGC 1


RESULT 11
US-10-067-125-54/c
; Sequence 54, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 54
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-54

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        576 CGTGAAGGCGCACCACGAGG 595
              ||||||||||||||||||||
Db         20 CGTGAAGGCGCACCACGAGG 1


RESULT 12
US-10-067-125-55/c
; Sequence 55, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 55
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-55

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        675 GACTTGTGGCAAGTGTCGAG 694
              ||||||||||||||||||||
Db         20 GACTTGTGGCAAGTGTCGAG 1


RESULT 13
US-10-067-125-56/c
; Sequence 56, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 56
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-56

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        751 CAGGAGCACGAGGTGCAGTG 770
              ||||||||||||||||||||
Db         20 CAGGAGCACGAGGTGCAGTG 1


RESULT 14
US-10-067-125-57/c
; Sequence 57, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 57
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-57

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        848 GGTCAGAGCTCCTGCAGAGG 867
              ||||||||||||||||||||
Db         20 GGTCAGAGCTCCTGCAGAGG 1


RESULT 15
US-10-067-125-58/c
```

; Sequence 58, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/10/067,125
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/167,109
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-067-125-58

Query Match 0.9%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 962 GCAGCCGGCAGCACCGGCTG 981
||||||||||||||||||||
Db 20 GCAGCCGGCAGCACCGGCTG 1

RESULT 16
US-10-067-125-59/c
; Sequence 59, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/10/067,125
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/167,109
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-067-125-59

Query Match 0.9%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1240 CTGAACGGCGACGGCACCGG 1259
||||||||||||||||||||
Db 20 CTGAACGGCGACGGCACCGG 1

RESULT 17
US-10-067-125-60/c
; Sequence 60, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/10/067,125
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/167,109
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-067-125-60

Query Match 0.9%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1387 GACGCCTTCAGGCCCGACGT 1406
||||||||||||||||||||
Db 20 GACGCCTTCAGGCCCGACGT 1

RESULT 18
US-10-067-125-61/c
; Sequence 61, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/10/067,125
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/167,109
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-067-125-61

Query Match 0.9%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1533 GGCCATTGTGGACCTGACAG 1552
||||||||||||||||||||
Db 20 GGCCATTGTGGACCTGACAG 1

RESULT 19
US-10-067-125-62/c
; Sequence 62, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/10/067,125
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/167,109
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228

```
; SEQ ID NO 62
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-62

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1590 GGCAGCCAGGCACAGCCGGC 1609
              ||||||||||||||||||||
Db         20 GGCAGCCAGGCACAGCCGGC 1


RESULT 20
US-10-067-125-63/c
; Sequence 63, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 63
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-63

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1685 GGTGTCGGCCTGCAGCCAAG 1704
              ||||||||||||||||||||
Db         20 GGTGTCGGCCTGCAGCCAAG 1


RESULT 21
US-10-067-125-64/c
; Sequence 64, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 64
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-64

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1789 GGCTGTGGTGGCATTGGCCG 1808
              ||||||||||||||||||||
Db         20 GGCTGTGGTGGCATTGGCCG 1


RESULT 22
US-10-067-125-65/c
; Sequence 65, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 65
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-65

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1916 CCATGTAGCAGGAGCACAGT 1935
              ||||||||||||||||||||
Db         20 CCATGTAGCAGGAGCACAGT 1


RESULT 23
US-10-067-125-66/c
; Sequence 66, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 66
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-66

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1994 GGCCTCCTGCTGGCCAGAGC 2013
              ||||||||||||||||||||
```

```
Db         20 GGCCTCCTGCTGGCCAGAGC 1


RESULT 24
US-10-067-125-67/c
; Sequence 67, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 67
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-67

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2117 CTTGGCCAGGCTGGCTGTGG 2136
             ||||||||||||||||||||
Db         20 CTTGGCCAGGCTGGCTGTGG 1


RESULT 25
US-10-067-125-68/c
; Sequence 68, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda F.
;  APPLICANT:  Cowsert, Lex M.
;  APPLICANT:  Monia, Brett P.
;  APPLICANT:  Xu, Xiaoxing S.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
;  FILE REFERENCE: ISPH-0321
;  CURRENT APPLICATION NUMBER: US/10/067,125
;  CURRENT FILING DATE:  2002-02-04
;  PRIOR APPLICATION NUMBER: 09/167,109
;  PRIOR FILING DATE: 1998-10-06
;  NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 68
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense sequence
US-10-067-125-68

  Query Match             0.9%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2221 TCCAGCTCACGAAGACAGAG 2240
             ||||||||||||||||||||
Db         20 TCCAGCTCACGAAGACAGAG 1


RESULT 26
US-10-726-148A-18/c
; Sequence 18, Application US/10726148A
; Publication No. US20040132157A1
; GENERAL INFORMATION:
;  APPLICANT: YOSHIMURA, Koji
;  APPLICANT:  HIKICHI, Yuichi
;  APPLICANT:  NISHIMURA, Atsushi
;  TITLE OF INVENTION: Novel Protein and DNA Thereof
;  FILE REFERENCE: PF613TD1
;  CURRENT APPLICATION NUMBER: US/10/726,148A
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: US 09/786,256
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: PCT/JP99/04766
;  PRIOR FILING DATE: 1999-09-02
;  PRIOR APPLICATION NUMBER: JP 10-250115
;  PRIOR FILING DATE: 1998-09-03
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Nucleic Acid Primer
US-10-726-148A-18

  Query Match             0.8%;  Score 19;  DB 17;  Length 30;
  Best Local Similarity   81.5%;  Pred. No. 3.2e+05;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        703 AGATTCCACGCCATCGGCTGCCTCGAG 729
              |||||||| | ||  |||| |||||||
Db         27 AGATTCCAAGTCAATGGCTTCCTCGAG 1


RESULT 27
US-09-950-335A-4/c
; Sequence 4, Application US/09950335A
; Publication No. US20020193330A1
; GENERAL INFORMATION:
;  APPLICANT: HONE, DAVID  M.
;  TITLE OF INVENTION: GENETICALLY ENGINEERED CO-EXPRESSION DNA VACCINES, CONSTRUCTION M
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: 4115-128
;  CURRENT APPLICATION NUMBER: US/09/950,335A
;  CURRENT FILING DATE:  2001-09-10
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic construct
US-09-950-335A-4

  Query Match             0.8%;  Score 18.6;  DB 9;  Length 29;
  Best Local Similarity   84.0%;  Pred. No. 4.1e+05;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1440 CATGAACATCGCAAGCGGCTGCCCC 1464
              || || ||||| ||||||| |||||
Db         25 CAAGATCATCGTAAGCGGCCGCCCC 1


RESULT 28
US-10-380-584-67
; Sequence 67, Application US/10380584
; Publication No. US20040014088A1
; GENERAL INFORMATION:
;  APPLICANT: Utermohlen, Joseph
;  APPLICANT:  Connaughton, John
;  TITLE OF INVENTION: Oligonucleotide Sequence Formula for Labeling Oligonucleotide Pro
;  TITLE OF INVENTION:  Proteins for In Situ Analysis
;  FILE REFERENCE: 355/001/PCT
```

```
;  CURRENT APPLICATION NUMBER: US/10/380,584
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 60/233,177
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide probe
US-10-380-584-67

  Query Match             0.8%;  Score 18.6;  DB 16;  Length 30;
  Best Local Similarity   84.0%;  Pred. No. 4.1e+05;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1836 GCTGCCCTTGCTGTCCTGTGCAGTG 1860
              |||| ||||||||||||  | |||
Db          6 GCTGTCCTTGCTGTCCTGCTCTGTG 30


RESULT 29
US-10-098-263B-67634
; Sequence 67634, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 67634
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-67634

  Query Match             0.8%;  Score 18.4;  DB 15;  Length 25;
  Best Local Similarity   95.0%;  Pred. No. 4.5e+05;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        747 ACAGCAGGAGCACGAGGTGC 766
              |||||||||||||| |||||
Db          5 ACAGCAGGAGCACGCGGTGC 24


RESULT 30
US-10-081-281-18
; Sequence 18, Application US/10081281
; Publication No. US20020151707A1
;   GENERAL INFORMATION:
;        APPLICANT: Kindsvogel, Wayne
;                   Gross, Jane A.
;                   Sheppard, Paul
;        TITLE OF INVENTION: Immune Mediators and Related Methods
;        NUMBER OF SEQUENCES: 121
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/081,281
;             FILING DATE: 20-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/261,811A
;             FILING DATE: 03-Mar-1999
;             APPLICATION NUMBER: US 08/480,002
;             FILING DATE: 07-JUN-1995
;             APPLICATION NUMBER: US 08/482,133
;             FILING DATE: 07-JUN-1995
;             APPLICATION NUMBER: US 08/483,241
;             FILING DATE: 07-JUN-1995
;             APPLICATION NUMBER: US 60/005,964
;             FILING DATE: 27-OCT-1995
;             APPLICATION NUMBER: US 08/657,581
;             FILING DATE: 07-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Parent, Annette S.
;             REGISTRATION NUMBER: 42,058
;             REFERENCE/DOCKET NUMBER: 014058-005630US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 18:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 30 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-081-281-18

  Query Match             0.8%;  Score 18.4;  DB 13;  Length 30;
  Best Local Similarity   78.6%;  Pred. No. 4.7e+05;
  Matches   22;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        328 CCAGATAATGCTGCCCGCAGGGAGGTGG 355
              |||  | || |  ||||||||||||||||
Db          2 CCACCTGATCCACCCCGCAGGGAGGTGG 29


RESULT 31
US-10-098-263B-42324/c
; Sequence 42324, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 42324
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-42324

  Query Match             0.8%;  Score 18.2;  DB 15;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 5.2e+05;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1638 GGTCTCACTGTACAAGTGGGCAG 1660
              |||||||||||| |||| || ||
Db         24 GGTCTCACTGTAGAAGTCGGGAG 2
```

```
RESULT 32
US-09-879-813-7
; Sequence 7, Application US/09879813
; Patent No. US20020155453A1
; GENERAL INFORMATION:
;  APPLICANT: Sale, Julian E.
;  APPLICANT:  Neuberger, Michael S.
;  APPLICANT:  Cumbers, Sarah J.
;  TITLE OF INVENTION: Method of Generating Diversity
;  FILE REFERENCE: 18396/2005
;  CURRENT APPLICATION NUMBER: US/09/879,813
;  CURRENT FILING DATE:  2001-06-11
;  PRIOR APPLICATION NUMBER: 09/828,717
;  PRIOR FILING DATE: 2001-06-04
;  PRIOR APPLICATION NUMBER: PCT/GB99/03358
;  PRIOR FILING DATE: 1999-10-08
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: primer
;   LOCATION: (1)..(29)
;   OTHER INFORMATION: oligonucleotide primer
US-09-879-813-7

  Query Match             0.8%;  Score 17.8;  DB 9;  Length 29;
  Best Local Similarity   75.9%;  Pred. No. 6.9e+05;
  Matches   22;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1691 GGCCTGCAGCCAAGTTCACTGTCACGGGG 1719
                || |||||| || ||||| || ||  |||
Db          1 GGACTGCAGTCAGGTTCAGTGGCAGTGGG 29


RESULT 33
US-09-828-717-7
; Sequence 7, Application US/09828717
; Publication No. US20030087236A1
; GENERAL INFORMATION:
;  APPLICANT: MRC Laboratory of Molecular Biology
;  TITLE OF INVENTION: Method for Generating Diversity
;  FILE REFERENCE: 18396/2002
;  CURRENT APPLICATION NUMBER: US/09/828,717
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: PCT/GB99/03358
;  PRIOR FILING DATE: 1998-10-09
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic primer
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(29)
;   OTHER INFORMATION: Synthetic primer
US-09-828-717-7

  Query Match             0.8%;  Score 17.8;  DB 10;  Length 29;
  Best Local Similarity   75.9%;  Pred. No. 6.9e+05;
  Matches   22;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1691 GGCCTGCAGCCAAGTTCACTGTCACGGGG 1719
                || |||||| || ||||| || ||  |||
Db          1 GGACTGCAGTCAGGTTCAGTGGCAGTGGG 29


RESULT 34
US-10-146-505-7
; Sequence 7, Application US/10146505
; Publication No. US20030108889A1
; GENERAL INFORMATION:
;  APPLICANT: Sale, Julian E.
;  APPLICANT:  Neuberger, Michael S.
;  APPLICANT:  Cumbers, Sarah J.
;  TITLE OF INVENTION: Method of Generating Diversity
;  FILE REFERENCE: 18396/2005B
;  CURRENT APPLICATION NUMBER: US/10/146,505
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/828,717
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 09/879,813
;  PRIOR FILING DATE: 2001-06-11
;  PRIOR APPLICATION NUMBER: PCT/GB99/03358
;  PRIOR FILING DATE: 1999-10-08
;  PRIOR APPLICATION NUMBER: GB 9822104.7
;  PRIOR FILING DATE: 1998-10-09
;  PRIOR APPLICATION NUMBER: GB 9901141.3
;  PRIOR FILING DATE: 1999-01-19
;  PRIOR APPLICATION NUMBER: GB 9913435.5
;  PRIOR FILING DATE: 1999-06-09
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: primer
US-10-146-505-7

  Query Match             0.8%;  Score 17.8;  DB 15;  Length 29;
  Best Local Similarity   75.9%;  Pred. No. 6.9e+05;
  Matches   22;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1691 GGCCTGCAGCCAAGTTCACTGTCACGGGG 1719
                || |||||| || ||||| || ||  |||
Db          1 GGACTGCAGTCAGGTTCAGTGGCAGTGGG 29


RESULT 35
US-10-157-382-4
; Sequence 4, Application US/10157382
; Publication No. US20030082668A1
; GENERAL INFORMATION:
;  APPLICANT: TAMAI, Katsuyuki
;  APPLICANT:  MIYAZAKI, Toshiaki
;  APPLICANT:  WADA, Emi
;  APPLICANT:  TATSUZAWA, Ayumi
;  TITLE OF INVENTION: METHOD FOR MEASURING THE ACTIVITY OF DEACETYLASE
;  TITLE OF INVENTION:  AND METHOD OF SCREENING FOR INHIBITORS AND ACCELERATORS
;  TITLE OF INVENTION:  OF THE ENZYME
;  FILE REFERENCE: M3-109PCT-US(CIP)
;  CURRENT APPLICATION NUMBER: US/10/157,382
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: PCT/JP00/08417
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: JP   1999-338565
;  PRIOR FILING DATE: 1999-11-29
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Artificially
;   OTHER INFORMATION: Synthesized Primer Sequence
US-10-157-382-4

  Query Match             0.8%;  Score 17.8;  DB 14;  Length 30;
  Best Local Similarity   75.9%;  Pred. No. 7e+05;
```

```
  Matches   22;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1389 CGCCTTCAGGCCCGACGTGACTTCATCCT 1417
              ||||| ||| || || |||| || ||||
Db          1 CGCCTCGAGGGCCAACTTGACCTCCTCCT 29


RESULT 36
US-10-098-263B-48292/c
; Sequence 48292, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48292
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-48292

  Query Match             0.8%;  Score 17.6;  DB 15;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 7.6e+05;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2164 TCAGACACTGTGTGGGAGGGCACA 2187
              || |||||||||| || || ||||
Db         25 TCGGACACTGTGTCGGTGGACACA 2


RESULT 37
US-10-098-263B-130463/c
; Sequence 130463, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 130463
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-130463

  Query Match             0.8%;  Score 17.6;  DB 15;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 7.6e+05;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1396 AGGCCCGACGTGACTTCATCCTCT 1419
              ||| ||||||| |||| ||||||
Db         24 AGGTCCGACGTATCTTCCTCCTCT 1


RESULT 38
US-10-098-263B-130464/c
; Sequence 130464, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 130464
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-130464

  Query Match             0.8%;  Score 17.6;  DB 15;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 7.6e+05;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1396 AGGCCCGACGTGACTTCATCCTCT 1419
              ||| ||||||| |||| ||||||
Db         24 AGGTCCGACGTTTCTTCCTCCTCT 1


RESULT 39
US-10-262-839-342
; Sequence 342, Application US/10262839
; Publication No. US20040038877A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, John,
;  APPLICANT:  Anderson, David W.,
;  APPLICANT:  Boldog, Ferenc,
;  APPLICANT:  Burgess, Catherine,
;  APPLICANT:  Catterton, Elina,
;  APPLICANT:  Edinger, Shlomit,
;  APPLICANT:  Ellerman, Karen,
;  APPLICANT:  Gerlach, Valerie,
;  APPLICANT:  Gorman, Linda,
;  APPLICANT:  Guo, Xiaojia,
;  APPLICANT:  Ji, Weizhen,
;  APPLICANT:  Kekuda, Ramesh,
;  APPLICANT:  Leach, Martin,
;  APPLICANT:  Li, Li,
;  APPLICANT:  Miller, Charles,
;  APPLICANT:  Patturajan, Meera,
;  APPLICANT:  Reiger, Daniel,
;  APPLICANT:  Rothenberg, Mark,
;  APPLICANT:  Shimkets, Richard,
;  APPLICANT:  Smithson, Glennda,
;  APPLICANT:  Spytek, Kimberly,
;  APPLICANT:  Taupier, Raymond, jr.,
;  APPLICANT:  Vernet, Corine,
;  APPLICANT:  Voss, Edward,
;  APPLICANT:  Zerhusen, Brian,
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
;  FILE REFERENCE: 21402-462A
;  CURRENT APPLICATION NUMBER: US/10/262,839
;  CURRENT FILING DATE:  2002-10-01
;  PRIOR APPLICATION NUMBER: 60/326,483
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: 60/327,917
;  PRIOR FILING DATE: 2001-10-09
;  PRIOR APPLICATION NUMBER: 60/328,029
;  PRIOR FILING DATE: 2001-10-09
;  PRIOR APPLICATION NUMBER: 60/328,056
;  PRIOR FILING DATE: 2001-10-09
;  PRIOR APPLICATION NUMBER: 60/381,101
;  PRIOR FILING DATE: 2002-05-16
;  PRIOR APPLICATION NUMBER: 60/371,972
;  PRIOR FILING DATE: 2002-04-12
;  PRIOR APPLICATION NUMBER: 60/327,342
;  PRIOR FILING DATE: 2001-10-05
;  PRIOR APPLICATION NUMBER: 60/328,044
;  PRIOR FILING DATE: 2001-10-09
;  PRIOR APPLICATION NUMBER: 60/328,849
```

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;  PRIOR FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: 60/374,738
;  PRIOR FILING DATE: 2002-04-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 367
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 342
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artifical Sequence:  Primer/Probe
US-10-262-839-342

  Query Match             0.8%;  Score 17.4;  DB 16;  Length 29;
  Best Local Similarity   77.8%;  Pred. No. 9e+05;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2087 TTGTCTGCACAGAGCTCTGGTCTGTGC 2113
              ||  |||||||  |||||  |||||||
Db          3 TTACCTGCACAAGGCTCTACTCTGTGC 29


RESULT 40
US-10-081-281-22
; Sequence 22, Application US/10081281
; Publication No. US20020151707A1
;   GENERAL INFORMATION:
;        APPLICANT: Kindsvogel, Wayne
;                   Gross, Jane A.
;                   Sheppard, Paul
;        TITLE OF INVENTION: Immune Mediators and Related Methods
;        NUMBER OF SEQUENCES: 121
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/081,281
;             FILING DATE: 20-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/261,811A
;             FILING DATE: 03-Mar-1999
;             APPLICATION NUMBER: US 08/480,002
;             FILING DATE: 07-JUN-1995
;             APPLICATION NUMBER: US 08/482,133
;             FILING DATE: 07-JUN-1995
;             APPLICATION NUMBER: US 08/483,241
;             FILING DATE: 07-JUN-1995
;             APPLICATION NUMBER: US 60/005,964
;             FILING DATE: 27-OCT-1995
;             APPLICATION NUMBER: US 08/657,581
;             FILING DATE: 07-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Parent, Annette S.
;             REGISTRATION NUMBER: 42,058
;             REFERENCE/DOCKET NUMBER: 014058-005630US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 22:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 30 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-081-281-22

  Query Match             0.8%;  Score 17.4;  DB 13;  Length 30;
  Best Local Similarity   77.8%;  Pred. No. 9.1e+05;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       328 CCAGATAATGCTGCCCGCAGGGAGGTG 354
             |||  | || |  ||||||||||||||
Db         2 CCACCTGATCCACCCCGCAGGGAGGTG 28


RESULT 41
US-10-343-810-12
; Sequence 12, Application US/10343810
; Publication No. US20040088760A1
; GENERAL INFORMATION:
;  APPLICANT: Allen, Randy D.
;  APPLICANT:  Song, Ping
;  TITLE OF INVENTION: GOSSYPIUM HIRSUTUM TISSUE-SPECIFIC PROMOTERS AND THEIR
;  TITLE OF INVENTION:  USE
;  FILE REFERENCE: 201304/1062
;  CURRENT APPLICATION NUMBER: US/10/343,810
;  CURRENT FILING DATE:  2003-10-24
;  PRIOR APPLICATION NUMBER: 60/223,496
;  PRIOR FILING DATE: 2000-08-07
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  primer
US-10-343-810-12

  Query Match             0.8%;  Score 17.4;  DB 16;  Length 30;
  Best Local Similarity   77.8%;  Pred. No. 9.1e+05;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       654 GAAGTTTCAGGACCACGTCAAGACTTG 680
             | |||||||| |||| ||| | | |||
Db         3 GCAGTTTCAGAACCAGGTCGATAGTTG 29


RESULT 42
US-10-244-647-1317
; Sequence 1317, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceutical, Inc.
;  APPLICANT:  Morrissey, David
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
;  TITLE OF INVENTION:  Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/060 (MBHB02-1000)
;  CURRENT APPLICATION NUMBER: US/10/244,647
;  CURRENT FILING DATE:  2003-04-14
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/393,924
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: PCT US02/09187
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/296,876
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1317
```

```
;   LENGTH: 23
;   TYPE: RNA
;   ORGANISM: Hepatitis B virus
US-10-244-647-1317

  Query Match             0.8%;  Score 17.2;  DB 15;  Length 23;
  Best Local Similarity   77.3%;  Pred. No. 9.7e+05;
  Matches   17;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        626 GCTGCGGCAAGAAGAAGATCCC 647
              ||: |  |||||||||||:|||
Db          2 GCUCCCUCAAGAAGAAGAUCCC 23


RESULT 43
US-10-098-263B-80858/c
; Sequence 80858, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 80858
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-80858

  Query Match             0.8%;  Score 17.2;  DB 15;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 9.9e+05;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        139 GAAGCCAAGTACCTGTGCTCCG 160
              | |||| ||||||||||| |||
Db         22 GGAGCCGAGTACCTGTGCACCG 1


RESULT 44
US-10-717-597-2427
; Sequence 2427, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Burczynski, Michael E.
;  APPLICANT:  Twine, Natalie C.
;  APPLICANT:  Dorner, Andrew J.
;  APPLICANT:  Trepicchio, William L.
;  APPLICANT:  Slonim, Donna K.
;  APPLICANT:  Stover, Jennifer A.
;  TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
;  FILE REFERENCE: AM101080L
;  CURRENT APPLICATION NUMBER: US/10/717,597
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 60/459,782
;  PRIOR FILING DATE: 2003-04-03
;  PRIOR APPLICATION NUMBER: US 60/427,982
;  PRIOR FILING DATE: 2002-11-21
;  NUMBER OF SEQ ID NOS: 4904
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2427
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-717-597-2427

  Query Match             0.8%;  Score 17.2;  DB 17;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 9.9e+05;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1678 TTGGGAGGGTGTCGGCCTGCAG 1699
              ||  |||||||||| |||||||
Db          3 TTCAGAGGGTGTCGTCCTGCAG 24


RESULT 45
US-09-320-337-42/c
; Sequence 42, Application US/09320337
; Patent No. US20010016352A1
;  GENERAL INFORMATION:
;    APPLICANT:  Bohinski, Robert J.,
;    APPLICANT:  Whitsett, Jeffrey A.
;    TITLE OF INVENTION:  Nucleic Acid Sequences Controlling
;    TITLE OF INVENTION:  Lung Cell - Specific Gene Expression
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM P160
;      OPERATING SYSTEM:  WINDOWS 95
;      SOFTWARE:  MS WORD 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/320,337
;      FILING DATE:  26-MAY-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/442,809
;      FILING DATE:  17-MAY-1995
;      APPLICATION NUMBER:  08/245,356
;      FILING DATE:  18-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  271010-447
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  973-994-1700
;      TELEFAX:  973-994-1744
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
US-09-320-337-42

  Query Match             0.8%;  Score 17.2;  DB 9;  Length 30;
  Best Local Similarity   73.3%;  Pred. No. 1e+06;
  Matches   22;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        847 GGGTCAGAGCTCCTGCAGAGGTGCGAGAGC 876
              | |||| | || |||||| ||  |||| ||
Db         30 GAGTCACACCTGCTGCAGTGGCTCGAGCGC 1


RESULT 46
US-10-215-112-4521
; Sequence 4521, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  TITLE OF INVENTION: Method of Genetic Analysis of Probes:
;  TITLE OF INVENTION:  Test3
;  FILE REFERENCE: 3119
;  CURRENT APPLICATION NUMBER: US/10/215,112
```

```
;  CURRENT FILING DATE:  2002-08-08
;  NUMBER OF SEQ ID NOS: 14936
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4521
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-4521

  Query Match             0.8%;  Score 17;  DB 14;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+06;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1242 GAACGGCGACGGCACCGGGCGAGGA 1266
             |||| || |||||||||  |||||
Db          1 GAACTTCGCCGGCACCGGTAGAGGA 25


RESULT 47
US-10-098-263B-8292
; Sequence 8292, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 8292
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-8292

  Query Match             0.8%;  Score 17;  DB 15;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+06;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        882 GAAGAAGACGGCCACTTTTGAGAAC 906
              || ||||||| ||||  ||||| ||
Db          1 GACGAAGACGACCACCCTTGAGTAC 25


RESULT 48
US-10-098-263B-32545/c
; Sequence 32545, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 32545
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-32545

  Query Match             0.8%;  Score 17;  DB 15;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+06;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2163 CTCAGACACTGTGTGGGAGGGCACA 2187
              ||| |||||||||  || || ||||
Db         25 CTCGGACACTGTGACGGTGGACACA 1


RESULT 49
US-10-098-263B-50938/c
; Sequence 50938, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 50938
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-50938

  Query Match             0.8%;  Score 17;  DB 15;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+06;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1892 AGTGGGAGCACATCCCAGCAGTGCC 1916
              ||| ||| || ||||||| |||| |
Db         25 AGTAGGATCAGATCCCAGAAGTGGC 1


RESULT 50
US-10-098-263B-54431/c
; Sequence 54431, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 54431
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-54431

  Query Match             0.8%;  Score 17;  DB 15;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+06;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1397 GGCCCGACGTGACTTCATCCTCTTT 1421
              || |  ||||| || ||||||||||
Db         25 GGTCACACGTGTCTCCATCCTCTTT 1


Search completed: November 20, 2004, 09:41:23
Job time : 1126 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 20, 2004, 03:17:09 ; Search time 7057 Seconds
(without alignments)
11680.129 Million cell updates/sec

Title: US-10-067-125-2
Perfect score: 2262
Sequence: 1 gaattccggcgcgctgcgac.....attaaaccattacaaatctc 2262

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 46458

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18.6	0.8	27	9	CG708102	CG708102 1119006E0
c 2	16.8	0.7	24	8	AZ770304	AZ770304 1M0571K14
c 3	16.8	0.7	29	8	AZ839016	AZ839016 2M0134O22
c 4	16.6	0.7	25	8	AZ460726	AZ460726 1M0266O10
c 5	16.4	0.7	29	8	AZ759919	AZ759919 1M0553H09
6	16.4	0.7	30	9	CG713193	CG713193 1119030G1
7	16.2	0.7	21	4	BM400027	BM400027 5009-0-65
8	16.2	0.7	28	8	AZ584848	AZ584848 1M0389I13
9	16	0.7	24	8	AZ936903	AZ936903 2M0193E20
c 10	16	0.7	25	8	AZ312923	AZ312923 1M0029L01
c 11	16	0.7	30	9	CG721980	CG721980 1119069G1
c 12	15.8	0.7	20	6	CD531709	CD531709 11M02 Ara
c 13	15.8	0.7	23	9	AG194875	AG194875 Pan trogl
14	15.8	0.7	28	8	BH907751	BH907751 SALK_0439
15	15.8	0.7	29	8	AZ479604	AZ479604 1M0300E21
16	15.8	0.7	29	8	AZ646100	AZ646100 1M0511P19
c 17	15.8	0.7	29	8	AZ854411	AZ854411 2M0158B05
18	15.6	0.7	25	1	AI757084	AI757084 EtESTea04
19	15.6	0.7	25	9	CG714622	CG714622 1119037E0
c 20	15.6	0.7	28	1	AI914763	AI914763 tr02a11.x
c 21	15.6	0.7	28	8	AZ307581	AZ307581 1M0009J09
c 22	15.6	0.7	29	8	AZ618807	AZ618807 1M0450N11
23	15.6	0.7	29	8	CC455120	CC455120 SALK_0553
c 24	15.4	0.7	24	8	AZ448189	AZ448189 1M0245A16
25	15.4	0.7	26	8	AZ447827	AZ447827 1M0245J08
26	15.4	0.7	28	1	AI756191	AI756191 EtESTea40
c 27	15.4	0.7	29	1	AU258464	AU258464 AU258464
28	15.4	0.7	29	4	BM399386	BM399386 5009-0-57
29	15.2	0.7	23	8	AZ789371	AZ789371 2M0037L01
30	15.2	0.7	26	4	BM397341	BM397341 5009-0-31
31	15.2	0.7	27	1	AU264485	AU264485 AU264485
32	15.2	0.7	27	9	TA264D03P	AL484006 T. brucei
c 33	15.2	0.7	28	1	AA877007	AA877007 ny49h08.s
c 34	15.2	0.7	28	1	AI804637	AI804637 tc81h03.x
35	15.2	0.7	28	8	AZ591936	AZ591936 1M0402J20
c 36	15.2	0.7	28	9	TA223E04P	AL480267 T. brucei
c 37	15.2	0.7	30	9	CR403528	CR403528 Arabidops
c 38	15.2	0.7	30	9	CC888357	CC888357 SALK_1517
c 39	15	0.7	23	8	AZ315824	AZ315824 1M0033O11
c 40	15	0.7	25	1	AI453742	AI453742 tj39g05.x
41	15	0.7	25	8	AZ595024	AZ595024 1M0407D23
c 42	15	0.7	25	9	AJ587447	AJ587447 Arabidops
c 43	15	0.7	25	9	CL693166	CL693166 PRI0160a_
c 44	15	0.7	27	9	CG708385	CG708385 1119009A0
c 45	15	0.7	29	1	AU257198	AU257198 AU257198
46	15	0.7	29	7	CO787079	CO787079 BL288A_F0
47	15	0.7	29	8	AZ618807	AZ618807 1M0450N11
c 48	15	0.7	30	8	AZ632209	AZ632209 1M0486B18
49	14.8	0.7	26	4	BM400727	BM400727 5009-0-78
c 50	14.8	0.7	27	1	AU008030	AU008030 AU008030

ALIGNMENTS

RESULT 1
CG708102
LOCUS CG708102 27 bp DNA linear GSS 20-OCT-2003
DEFINITION 1119006E02.2EL_y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
ACCESSION CG708102
VERSION CG708102.1 GI:37734008
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 27)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119006 row: E column: 02
Class: transposon-tagged.
FEATURES Location/Qualifiers
source 1. .27
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 0.8%; Score 18.6; DB 9; Length 27;
Best Local Similarity 84.0%; Pred. No. 1.6e+07;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy        629 GCGGCAAGAAGAAGATCCCCCGGGA 653
              ||||| ||||| ||| |||| ||||
Db          2 GCGGCGAGAAGCAGACCCCCGGGGA 26
```

RESULT 2
AZ770304/c
LOCUS AZ770304 24 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0571K14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0571K14 R, genomic survey sequence.
ACCESSION AZ770304
VERSION AZ770304.1 GI:12891351
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0571 row: K column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
FEATURES Location/Qualifiers
source 1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0571K14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.7%; Score 16.8; DB 8; Length 24;
Best Local Similarity 90.0%; Pred. No. 4e+07;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        988 GACAAGATTGAAGCCCTGAG 1007
              |||||| | ||||||||||||
Db         24 GACAAGTTCGAAGCCCTGAG 5
```

RESULT 3
AZ839016/c
LOCUS AZ839016 29 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0134O22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0134O22 R, genomic survey sequence.
ACCESSION AZ839016
VERSION AZ839016.1 GI:13008924
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0134 row: O column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0134O22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

```
  Query Match             0.7%;  Score 16.8;  DB 8;  Length 29;
  Best Local Similarity   75.0%;  Pred. No. 4.1e+07;
  Matches   21;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2180 AGGGCACAGCACAGCTGCGGGTAAAGTG 2207
              | | || ||||| |||| |||| | |||
Db         28 AAGCCAGAGCACGGCTGGGGGTCAGGTG 1
```

RESULT 4
AZ460726/c
LOCUS AZ460726 25 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0266O10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0266O10 F, genomic survey sequence.
ACCESSION AZ460726
VERSION AZ460726.1 GI:10618851
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0266 row: O column: 10
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
FEATURES Location/Qualifiers
source 1. .25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0266O10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

```
  Query Match             0.7%;  Score 16.6;  DB 8;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 4.5e+07;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1579 TGGGGGTTGGGGGCAGCCAGGCA 1601
              ||||||||||| | || |||| |
Db         23 TGGGGGTTGGGTGAAGGCAGGGA 1
```

RESULT 5
AZ759919/c
LOCUS AZ759919 29 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0553H09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0553H09 F, genomic survey sequence.
ACCESSION AZ759919
VERSION AZ759919.1 GI:12867200
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0553 row: H column: 09
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0553H09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.7%; Score 16.4; DB 8; Length 29;
Best Local Similarity 76.9%; Pred. No. 5.1e+07;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy        338 CTGCCCGCAGGGAGGTGGAGAGCCTG 363
              ||||| ||||| |  |||| | ||||
Db         26 CTGCCTGCAGGAACCTGGAAATCCTG 1
```

RESULT 6
CG713193
LOCUS CG713193 30 bp DNA linear GSS 20-OCT-2003
DEFINITION 1119030G10.2EL_y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
ACCESSION CG713193
VERSION CG713193.1 GI:37739099
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 30)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119030 row: G column: 10
Class: transposon-tagged.
FEATURES Location/Qualifiers
source 1. .30
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 0.7%; Score 16.4; DB 9; Length 30;
Best Local Similarity 76.9%; Pred. No. 5.1e+07;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy        627 CTGCGGCAAGAAGAAGATCCCCCGGG 652
              | ||||| ||||| | | |||| |||
Db          5 CAGCGGCGAGAAGCAAACCCCCGGGG 30
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RESULT 7
BM400027
LOCUS BM400027 21 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-65-A06.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM400027
VERSION BM400027.1 GI:18200080
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 21)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .21
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 0.7%; Score 16.2; DB 4; Length 21;
Best Local Similarity 85.7%; Pred. No. 5.4e+07;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        829 GGAGACCAGAGCCACGCGGGG 849
              ||| | | ||||||||||||||
Db          1 GGAAAACTGAGCCACGCGGGG 21
```

RESULT 8
AZ584848
LOCUS AZ584848 28 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0389I13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0389I13 R, genomic survey sequence.
ACCESSION AZ584848
VERSION AZ584848.1 GI:11706145
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

```
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0389  row: I  column: 13
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 28.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0389I13"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             0.7%;  Score 16.2;  DB 8;  Length 28;
  Best Local Similarity   85.7%;  Pred. No. 5.7e+07;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1574 GTGTCTGGGGGTTGGGGGCAG 1594
              ||||||||||   ||||||||
Db             1 GTGTCTGGGGTCCGGGGGCAG 21


RESULT 9
AZ936903
LOCUS       AZ936903                 24 bp    DNA     linear   GSS 26-APR-2001
DEFINITION  2M0193E20R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0193E20 R, genomic survey sequence.
ACCESSION   AZ936903
VERSION     AZ936903.1  GI:13795484
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
```

```
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0193  row: E  column: 20
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0193E20"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             0.7%;  Score 16;  DB 8;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 6.1e+07;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1860 GAAGGGAGAGGCCCTGGGTGGGGG 1883
              ||||||||||||||  | | | |||
Db             1 GAAGGGAGAGGCCTGGTGGGAGGG 24


RESULT 10
AZ312923/c
LOCUS       AZ312923                 25 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0029L01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0029L01 F, genomic survey sequence.
ACCESSION   AZ312923
VERSION     AZ312923.1  GI:10357337
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
```

```
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0029  row: L  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0029L01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynuclectide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             0.7%;  Score 16;  DB 8;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 6.2e+07;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1879 GGGGGACACTCAGAGTGGGAGCAC 1902
              ||| ||||  |||||||| || ||
Db         25 GGGTGACATCCAGAGTGGCAGTAC 2


RESULT 11
CG721980/c
LOCUS       CG721980                  30 bp    DNA     linear   GSS 20-OCT-2003
DEFINITION  1119069G12.1EL_y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
            survey sequence.
ACCESSION   CG721980
VERSION     CG721980.1  GI:37756386
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Walbot,V.
  TITLE     Maize genomic sequences found using engineered RescueMu transposon
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Very probable ligation site of ends cut by single endonuclease.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1119069  row: G  column: 12
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="mixed background W23/A188/B73/K55"
                     /db_xref="taxon:4577"
                     /tissue_type="leaf"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="1119 - RescueMu Grid AA"
                     /note="Organ: leaf; Vector: RescueMu (engineered from
                     pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
                     RescueMu is a 4.9 kb, modified maize Mu transposon
                     designed to allow plasmid rescue from total genomic DNA.
                     Mu elements insert preferentially into transcription
                     units. For more information on RescueMu, go to the web
                     site 'www.zmdb.iastate.edu' and follow the links for
                     'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
                     was extracted from leaf strips, double digested using
                     BamHI and BglII, and ligated to form circular plasmids.
                     DH10B cells were transformed and then screened on LB
                     plates with ampicillin."
ORIGIN

  Query Match             0.7%;  Score 16;  DB 9;  Length 30;
  Best Local Similarity   79.2%;  Pred. No. 6.3e+07;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        605 AGTTCCCCTTAACTTGTGACGGCT 628
              |||| ||| ||  ||| |||||||
Db         30 AGTTGCCCGTACGTTGCGACGGCT 7


RESULT 12
CD531709/c
LOCUS       CD531709                  20 bp    mRNA    linear   EST 31-DEC-2003
DEFINITION  11M02 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA
            3', mRNA sequence.
ACCESSION   CD531709
VERSION     CD531709.1  GI:40451721
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Guo,Y., Cai,Z. and Gan,S.
  TITLE     Transcriptome of Arabidopsis leaf senescence
  JOURNAL   Plant Cell Environ. 27 (5), 521-549 (2004)
COMMENT     Contact: Susheng Gan
            Department of Horticulture
            Cornell University
            119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
            Tel: 607 254 5418
            Fax: 607 255 0599
            Email: sg288@cornell.edu
            Insert Length: 20   Std Error: 0.00
            Seq primer: T7
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /ecotype="Landsberg erecta"
```

```
                     /db_xref="taxon:3702"
                     /tissue_type="Leaf"
                     /dev_stage="Yellow Leaf With Greenish Base Area"
                     /lab_host="E. coli"
                     /clone_lib="Arabidopsis Leaf Senescence Library"
                     /note="Organ: Rosette Leaf; Vector: pBluscript SKII+;
                     Site_1: EcoRI; Site_2: EcoRI; Senescent rosette leaves #5
                     and #6 (counted from the bottom) were  harvested and
                     immediately frozen in liquid N2. The leaves were  visibly
                     yellow excepted for the leaf base areas that were still
                     greenish. "
ORIGIN

  Query Match             0.7%;  Score 15.8;  DB 6;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 6.7e+07;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1530 CAAGGCCATTGTGGACCTG 1548
              ||||||||||||  || |||
Db         20 CAAGGCCATTGTTGAGCTG 2


RESULT 13
AG194875/c
LOCUS       AG194875                  23 bp    DNA     linear   GSS 06-MAR-2004
DEFINITION  Pan troglodytes DNA, clone: RP43-073F19.TJ, genomic survey
            sequence.
ACCESSION   AG194875
VERSION     AG194875.1  GI:45227051
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     BAC end sequences of Library RP-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 23)
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: TJ
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-073F19.TJ"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match             0.7%;  Score 15.8;  DB 9;  Length 23;
  Best Local Similarity   89.5%;  Pred. No. 6.8e+07;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1919 TGTAGCAGGAGCACAGTGG 1937
              |||||||| |||||| |||
Db         22 TGTAGCAGCAGCACAATGG 4


RESULT 14
BH907751
LOCUS       BH907751                  28 bp    DNA     linear   GSS 04-SEP-2002
DEFINITION  SALK_043999.44.90.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_043999.44.90.x, genomic
            survey sequence.
ACCESSION   BH907751
VERSION     BH907751.1  GI:22720684
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within 300 bases of the 5' end of
            At1g47650.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_043999.44.90.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match             0.7%;  Score 15.8;  DB 8;  Length 28;
  Best Local Similarity   74.1%;  Pred. No. 7e+07;
  Matches   20;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        283 ATATATGAAGAAGGCATTTCTATTTTA 309
              | |||| | |||||| ||||| || |
Db          2 AGATATTATGAAGGCTTTTCTCATTAA 28


RESULT 15
AZ479604
LOCUS       AZ479604                  29 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0300E21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0300E21 F, genomic survey sequence.
ACCESSION   AZ479604
VERSION     AZ479604.1  GI:10639113
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

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REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0300  row: E  column: 21
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0300E21"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             0.7%;  Score 15.8;  DB 8;  Length 29;
  Best Local Similarity   89.5%;  Pred. No. 7e+07;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1573 GGTGTCTGGGGGTTGGGGG 1591
              || ||||||||| ||||||
Db         11 GGAGTCTGGGGGGTGGGGG 29


RESULT 16
AZ646100
LOCUS       AZ646100                 29 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0511P19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0511P19 R, genomic survey sequence.
ACCESSION   AZ646100
VERSION     AZ646100.1  GI:11776226
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0511  row: P  column: 19
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0511P19"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             0.7%;  Score 15.8;  DB 8;  Length 29;
  Best Local Similarity   74.1%;  Pred. No. 7e+07;
  Matches   20;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2109 TGTGCCACCTTGGCCAGGCTGGCTGTG 2135
              || ||||||   |||| |||  |||||
Db          2 TGCGCCACCACTGCCAAGCTTTCTGTG 28


RESULT 17
AZ854411/c
LOCUS       AZ854411                 29 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0158B05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0158B05 F, genomic survey sequence.
ACCESSION   AZ854411
VERSION     AZ854411.1  GI:13043500
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0158  row: B  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0158B05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             0.7%;  Score 15.8;  DB 8;  Length 29;
  Best Local Similarity   74.1%;  Pred. No. 7e+07;
  Matches   20;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        732 GGTAGAGGGTGAGAAACAGCAGGAGCA 758
              || | |||  ||||| ||| |||| ||
Db         28 GGAACAGGAGGAGAAGCAGGAGGAACA 2


RESULT 18
AI757084
LOCUS       AI757084                  25 bp    mRNA    linear   EST 18-JAN-2000
DEFINITION  EtESTea04d05.y1 Eimeria M5-6 Merozoite stage Eimeria tenella cDNA
            5' similar to TR:Q64526 Q64526 ULTRA-HIGH SULPHUR KERATIN. ;, mRNA
            sequence.
ACCESSION   AI757084
VERSION     AI757084.1  GI:5150807
KEYWORDS    EST.
SOURCE      Eimeria tenella
  ORGANISM  Eimeria tenella
            Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
            Eimeria.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Liberator,P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T.,
            Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B.,
            Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D.,
            Harvey,N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,T.,
            Jackson,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and
            Sibley,D.
  TITLE     WashU-Merck Eimeria tenella project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: David Sibley, Ph.D.
            WashU-Merck Eimeria tenella project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Contact David Sibley (toxoest@borcim.wustl.edu) for further
            information relating to organism, libraries, or clone availability.
            Seq primer: -40RP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Eimeria tenella"
                     /mol_type="mRNA"
                     /strain="LS18"
                     /db_xref="taxon:5802"
                     /dev_stage="Merozoite"
                     /lab_host="SOLR E. coli"
                     /clone_lib="Eimeria M5-6 Merozoite stage"
                     /note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; Merozoites were obtained from ceacal scrapings of
                     chickens infected with E. tenella.  The library may
                     contain a small percentage of host or bacterial
                     contaminents.  cDNA was synthesized from poly mRNA using
                     an oligo-dT primer containing a XhoI site.  Following
                     second strand synthesis, EcoRI adapters were ligated to
                     the cDNA and products were size-selected on Sephacryl
                     S500.  cDNAs were digested with EcoRI/XhoI and cloned into
                     lambda Zap II (Stratagene).  Clones were converted to
                     phagemids by mass excision using ExAssist helper phage and
                     SOLR cells (Stratagene ).  Insert sizes range from 0.7-1.5
                     kb."
ORIGIN

  Query Match             0.7%;  Score 15.6;  DB 1;  Length 25;
  Best Local Similarity   81.8%;  Pred. No. 7.6e+07;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1452 AAGCGGCTGCCCCCTCTTCTGC 1473
              ||||  |||||||| || ||||
Db          4 AAGCCCCTGCCCCCCCTGCTGC 25


RESULT 19
CG714622
LOCUS       CG714622                  25 bp    DNA     linear   GSS 20-OCT-2003
DEFINITION  1119037E09.2EL_y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
            survey sequence.
ACCESSION   CG714622
VERSION     CG714622.1  GI:37741156
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Walbot,V.
  TITLE     Maize genomic sequences found using engineered RescueMu transposon
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
```

```
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Possible ligation site of ends cut by 2 different endonucleases.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1119037  row: E  column: 09
            Class: transposon-tagged.
FEATURES              Location/Qualifiers
     source           1. .25
                      /organism="Zea mays"
                      /mol_type="genomic DNA"
                      /cultivar="mixed background W23/A188/B73/K55"
                      /db_xref="taxon:4577"
                      /tissue_type="leaf"
                      /dev_stage="adult"
                      /lab_host="DH10B"
                      /clone_lib="1119 - RescueMu Grid AA"
                      /note="Organ: leaf; Vector: RescueMu (engineered from
                      pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
                      RescueMu is a 4.9 kb, modified maize Mu transposon
                      designed to allow plasmid rescue from total genomic DNA.
                      Mu elements insert preferentially into transcription
                      units. For more information on RescueMu, go to the web
                      site 'www.zmdb.iastate.edu' and follow the links for
                      'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
                      was extracted from leaf strips, double digested using
                      BamHI and BglII, and ligated to form circular plasmids.
                      DH10B cells were transformed and then screened on LB
                      plates with ampicillin."
ORIGIN

  Query Match             0.7%;  Score 15.6;  DB 9;  Length 25;
  Best Local Similarity   81.8%;  Pred. No. 7.6e+07;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        970 CAGCACCGGCTGGACCAAGACA 991
              ||||||||| |||||||   ||
Db          1 CAGCACCGGTTGGACCAGTCCA 22


RESULT 20
AI914763/c
LOCUS       AI914763                 28 bp    mRNA    linear   EST 28-JUL-1999
DEFINITION  tr02a11.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2217116 3'
            similar to TR:O16161 O16161 PRECOLLAGEN P PRECURSOR. ;, mRNA
            sequence.
ACCESSION   AI914763
VERSION     AI914763.1  GI:5634618
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .28
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2217116"
                      /tissue_type="tumor, 5 pooled (see description)"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Ov23"
                      /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.35 kb. Tumor types include: mixed
                      Mullerian tumor, papillary serous, clear cell, spindle
                      cell.  All are primary tumors, metastasis positive. Life
                      Technologies catalog #: 11534-013"
ORIGIN

  Query Match             0.7%;  Score 15.6;  DB 1;  Length 28;
  Best Local Similarity   81.8%;  Pred. No. 7.7e+07;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1661 GGGCCCCGCTTGGGCGCTTGGG 1682
              ||||||| ||| | | ||||||
Db         22 GGGCCCCCCTTTGCCCCTTGGG 1


RESULT 21
AZ307581/c
LOCUS       AZ307581                 28 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0009J09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0009J09 R, genomic survey sequence.
ACCESSION   AZ307581
VERSION     AZ307581.1  GI:10346724
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0009  row: J  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 28.
FEATURES              Location/Qualifiers
     source           1. .28
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0009J09"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.7%; Score 15.6; DB 8; Length 28;
Best Local Similarity 81.8%; Pred. No. 7.7e+07;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 734 TAGAGGGTGAGAAACAGCAGGA 755
Db 22 TGGATGGTGGGAAACAGGAGGA 1

RESULT 22
AZ618807/c
LOCUS AZ618807 29 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0450N11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0450N11 R, genomic survey sequence.
ACCESSION AZ618807
VERSION AZ618807.1 GI:11740997
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0450 row: N column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0450N11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.7%; Score 15.6; DB 8; Length 29;
Best Local Similarity 81.8%; Pred. No. 7.8e+07;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1174 CCCGCCATCTTCTCCCCAGCCT 1195
Db 28 CCCACCATCACCTCCCCAGTCT 7

RESULT 23
CC455120
LOCUS CC455120 29 bp DNA linear GSS 30-MAY-2003
DEFINITION SALK_055370.47.35.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_055370.47.35.x, genomic survey sequence.
ACCESSION CC455120
VERSION CC455120.1 GI:31214989
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 29)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1. .29
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_055370.47.35.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 0.7%; Score 15.6; DB 8; Length 29;

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  Best Local Similarity   81.8%;  Pred. No. 7.8e+07;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        279 GGGCATATATGAAGAAGGCATT 300
              | |  ||| ||||||||||||||
Db          7 GTGTTTATGTGAAGAAGGCATT 28


RESULT 24
AZ448189/c
LOCUS       AZ448189                 24 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0245A16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0245A16 R, genomic survey sequence.
ACCESSION   AZ448189
VERSION     AZ448189.1  GI:10600741
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0245  row: A  column: 16
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0245A16"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             0.7%;  Score 15.4;  DB 8;  Length 24;

  Best Local Similarity   94.1%;  Pred. No. 8.4e+07;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2177 GGGAGGGCACAGCACAG 2193
              ||||||||||| ||||||
Db         24 GGGAGGGCACTGCACAG 8


RESULT 25
AZ447827
LOCUS       AZ447827                 26 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0245J08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0245J08 F, genomic survey sequence.
ACCESSION   AZ447827
VERSION     AZ447827.1  GI:10600013
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0245  row: J  column: 08
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 26.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0245J08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             0.7%;  Score 15.4;  DB 8;  Length 26;
```

```
  Best Local Similarity   76.0%;  Pred. No. 8.5e+07;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1266 AACACACCTGTCCCTCTTCTTTGTG 1290
              || ||   |||||||| |||| |||
Db          1 AATACTGATGTCCCTCGTCTTGGTG 25


RESULT 26
AI756191
LOCUS       AI756191                  28 bp    mRNA    linear   EST 18-JAN-2000
DEFINITION  EtESTea40h07.y1 Eimeria S5-2 Sporozoite stage Eimeria tenella cDNA
            5' similar to TR:Q64507 Q64507 SERINE 1 ULTRA HIGH SULFUR PROTEIN.
            ;, mRNA sequence.
ACCESSION   AI756191
VERSION     AI756191.1  GI:5149914
KEYWORDS    EST.
SOURCE      Eimeria tenella
  ORGANISM  Eimeria tenella
            Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
            Eimeria.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Liberator,P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T.,
            Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B.,
            Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D.,
            Harvey,N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,T.,
            Jackson,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and
            Sibley,D.
  TITLE     WashU-Merck Eimeria tenella project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: David Sibley, Ph.D.
            WashU-Merck Eimeria tenella project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Contact David Sibley (toxoest@borcim.wustl.edu) for further
            information relating to organism, libraries, or clone availability.
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40RP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Eimeria tenella"
                     /mol_type="mRNA"
                     /strain="LS18"
                     /db_xref="taxon:5802"
                     /dev_stage="Sporozoite"
                     /lab_host="SOLR E. coli"
                     /clone_lib="Eimeria S5-2 Sporozoite stage"
                     /note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; Sporozoites were obtained from in vitro sporulated
                     and excysted oocysts of E. tenella grown in chickens.
                     cDNA was synthesized from poly mRNA using an oligo-dT
                     primer containing a XhoI site. Following second strand
                     synthesis, EcoRI adapters were ligated to the cDNA and
                     products were size-selected on Sephacryl S500. cDNAs were
                     digested with EcoRI/XhoI and cloned into lambda Zap II
                     (Stratagene). Clones were converted to phagemids by mass
                     excision using ExAssist helper phage and SOLR cells
                     (Stratagene ). Insert sizes range from 1.2-2.9 kb."
ORIGIN

  Query Match             0.7%;  Score 15.4;  DB 1;  Length 28;
  Best Local Similarity   76.0%;  Pred. No. 8.6e+07;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        765 GCAGTGGCTGCGGGAGCACCTGGCC 789
              ||||  ||||||| |||||   |||
Db          2 GCAGCTGCTGCGGCAGCACAGAGCC 26


RESULT 27
AU258464/c
LOCUS       AU258464                  29 bp    mRNA    linear   EST 25-APR-2002
DEFINITION  AU258464 3'-directed mouse cDNA library Mus musculus cDNA clone
            BED0013042 3', mRNA sequence.
ACCESSION   AU258464
VERSION     AU258464.1  GI:20324052
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Kato,K. and Matoba,R.
  TITLE     Generation of expressed sequence tags from mouse brain
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
            Tel: 81-743-72-5581
            Fax: 81-743-72-5589
            Email: kkato@bs.aist-nara.ac.jp,
            URL:http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="BED0013042"
                     /tissue_type="brain"
                     /clone_lib="3'-directed mouse cDNA library"
ORIGIN

  Query Match             0.7%;  Score 15.4;  DB 1;  Length 29;
  Best Local Similarity   76.0%;  Pred. No. 8.6e+07;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        740 GTGAGAAACAGCAGGAGCACGAGGT 764
              ||| || |||||||||  | ||| |
Db         26 GTGGGAGACAGCAGGAAGAAGAGAT 2


RESULT 28
BM399386
LOCUS       BM399386                  29 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-57-C01.t.2 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM399386
VERSION     BM399386.1  GI:18199439
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
```

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                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

  Query Match             0.7%;  Score 15.4;  DB 4;  Length 29;
  Best Local Similarity   76.0%;  Pred. No. 8.6e+07;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        741 TGAGAAACAGCAGGAGCACGAGGTG 765
              ||| ||| |||  || |||| ||||
Db          1 TGACAAAAAGCTTGACCACGCGGTG 25


RESULT 29
AZ789371
LOCUS       AZ789371                 23 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0037L01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0037L01 F, genomic survey sequence.
ACCESSION   AZ789371
VERSION     AZ789371.1  GI:12930098
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0037  row: L  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0037L01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             0.7%;  Score 15.2;  DB 8;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 9.3e+07;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        686 AGTGTCGAGTCCCTTGCAGA 705
              ||||  || ||||||||||||
Db          4 AGTGGTGATTCCCTTGCAGA 23


RESULT 30
BM397341
LOCUS       BM397341                 26 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-31-D02.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM397341
VERSION     BM397341.1  GI:18197394
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

  Query Match             0.7%;  Score 15.2;  DB 4;  Length 26;
  Best Local Similarity   85.0%;  Pred. No. 9.4e+07;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        830 GAGACCAGAGCCACGCGGGG 849
              || | | ||||||||||||||
Db          1 GACAACTGAGCCACGCGGGG 20


RESULT 31
AU264485
LOCUS       AU264485                 27 bp    mRNA    linear   EST 26-APR-2004
DEFINITION  AU264485 VS Dictyostelium discoideum cDNA clone VSD734 5', mRNA
            sequence.
ACCESSION   AU264485
VERSION     AU264485.1  GI:20523283
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
```

```
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Kohara,Y., Koriki,E., Ochiai,H.,
            Maeda,M., Williams,J.G., Takeuchi,I. and Tanaka,Y.
  TITLE     Analyses of cDNAs from growth and slug stages of Dictyostelium
            discoideum
  JOURNAL   Nucleic Acids Res. 32 (5), 1647-1653 (2004)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSD734"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"
ORIGIN

  Query Match             0.7%;  Score 15.2;  DB 1;  Length 27;
  Best Local Similarity   85.0%;  Pred. No. 9.5e+07;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1444 AACATCGCAAGCGGCTGCCC 1463
              | |||||| |||||| ||||
Db          6 AGCATCGCGAGCGGCCGCCC 25


RESULT 32
TA264D03P
LOCUS       TA264D03P                 27 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 264d03, forward sequence,
            genomic survey sequence.
ACCESSION   AL484006
VERSION     AL484006.1  GI:11849966
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="264d03"
ORIGIN

  Query Match             0.7%;  Score 15.2;  DB 9;  Length 27;
  Best Local Similarity   85.0%;  Pred. No. 9.5e+07;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        541 TGCCGGCATTGCCGGGCACC 560
              |||| || ||||||||||| |
Db          2 TGCCCGCCTTGCCGGGCAAC 21


RESULT 33
AA877007/c
LOCUS       AA877007                  28 bp    mRNA    linear   EST 25-MAR-1998
DEFINITION  ny49h08.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1275135
            similar to TR:Q13765 Q13765 NASCENT POLYPEPTIDE ASSOCIATED COMPLEX
            ALPHA SUBUNIT. ;, mRNA sequence.
ACCESSION   AA877007
VERSION     AA877007.1  GI:2986084
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
            Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1275135"
                     /sex="male"
                     /tissue_type="metastatic prostate bone lesion"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Pr12"
                     /note="Vector: pAMP10; mRNA made from metastatic prostate
                     lesion of the bone, cDNA made by  oligo-dT priming.
                     Non-directionally cloned.  Size-selected on agarose  gel,
                     average insert size 600 bp.  Library made by D. Krizman,
                     NIH."
ORIGIN

  Query Match             0.7%;  Score 15.2;  DB 1;  Length 28;
  Best Local Similarity   71.4%;  Pred. No. 9.5e+07;
  Matches   20;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       1635 CAGGGTCTCACTGTACAAGTGGGCAGGG 1662
              |||  ||  |||||||||| ||  || |
Db         28 CAGACTCCAACTGTACAAGAGGAGAGTG 1


RESULT 34
AI804637/c
LOCUS       AI804637                  28 bp    mRNA    linear   EST 13-DEC-1999
DEFINITION  tc81h03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2072597 3'
```

similar to TR:Q04117 Q04117 SALIVARY PROLINE-RICH PROTEIN RP4 PRECURSOR. ;contains element MSR1 repetitive element ;, mRNA sequence.
ACCESSION AI804637
VERSION AI804637.1 GI:5370109
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 28)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 304 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2072597"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_CLL1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATTGCTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN

Query Match 0.7%; Score 15.2; DB 1; Length 28;
Best Local Similarity 71.4%; Pred. No. 9.5e+07;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1563 GCCCCCTACTGGTGTCTGGGGGTTGGGG 1590
| |||| ||| | |||||| |||||
Db 28 GGCCCCCCGGGGTTTTTGGGGGGTGGGG 1

RESULT 35
AZ591936
LOCUS AZ591936 28 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0402J20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0402J20 F, genomic survey sequence.
ACCESSION AZ591936
VERSION AZ591936.1 GI:11714126
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0402 row: J column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
FEATURES Location/Qualifiers
source 1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0402J20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN

Query Match 0.7%; Score 15.2; DB 8; Length 28;
Best Local Similarity 85.0%; Pred. No. 9.5e+07;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1042 CTCAAGGACCTGGCGATGGC 1061
|| |||||||||| |||||
Db 7 CTGAAGGACCTGGATATGGC 26

RESULT 36
TA223E04P/c
LOCUS TA223E04P 28 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 223e04, forward sequence, genomic survey sequence.
ACCESSION AL480267
VERSION AL480267.1 GI:11846047
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 28)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .28
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="223e04"
ORIGIN

Query Match 0.7%; Score 15.2; DB 9; Length 28;
Best Local Similarity 85.0%; Pred. No. 9.5e+07;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1294 ATGAAGGGCCCGAATGACGC 1313
||| ||||||| ||| ||||
Db 27 ATGGAGGGCCCAAATCACGC 8

RESULT 37
CR403528/c
LOCUS CR403528 30 bp DNA linear GSS 02-MAY-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-864A05-025981, genomic survey sequence.
ACCESSION CR403528
VERSION CR403528.1 GI:46944256
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 30)
AUTHORS Strizhov,N., Rosso,M.G., Li,Y. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5g35790. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES Location/Qualifiers
source 1. .30
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-864A05-025981"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
ORIGIN

Query Match 0.7%; Score 15.2; DB 9; Length 30;
Best Local Similarity 71.4%; Pred. No. 9.6e+07;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 515 ACGAGTGCCCGGAGAGAAGCCTGAGCTG 542
|| ||| || | || | | ||||||||
Db 29 ACAAGTTTCCTGGGACATGTCTGAGCTG 2

RESULT 38
CC888357/c
LOCUS CC888357 30 bp DNA linear GSS 31-JUL-2003
DEFINITION SALK_151745.32.65.n Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_151745.32.65.n, genomic survey sequence.
ACCESSION CC888357
VERSION CC888357.1 GI:33364906
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 30)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At3g51240.
Class: TDNA tagged.
FEATURES Location/Qualifiers

```
     source          1. .30
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_151745.32.65.n"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match             0.7%;  Score 15.2;  DB 9;  Length 30;
  Best Local Similarity   71.4%;  Pred. No. 9.6e+07;
  Matches   20;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        615 AACTTGTGACGGCTGCGGCAAGAAGAAG 642
              | ||||||| | |||  | | ||||| |
Db         30 AGCTTGTGATGACTGACGAACGAAGAGG 3


RESULT 39
AZ315824/c
LOCUS       AZ315824                 23 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0033O11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0033O11 F, genomic survey sequence.
ACCESSION   AZ315824
VERSION     AZ315824.1  GI:10363039
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0033  row: O  column: 11
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0033O11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             0.7%;  Score 15;  DB 8;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 1e+08;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        125 TGGGGACCAAGCTGGAAGCCAAG 147
              |||||| || |||  |||| |||
Db         23 TGGGGAACATGCTTAAAGCAAAG 1


RESULT 40
AI453742/c
LOCUS       AI453742                 25 bp    mRNA    linear   EST 09-MAR-1999
DEFINITION  tj39g05.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2143928 3'
            similar to SW:LB4D_HUMAN Q14914 NADP-DEPENDENT LEUKOTRIENE B4
            12-HYDROXYDEHYDROGENASE ;, mRNA sequence.
ACCESSION   AI453742
VERSION     AI453742.1  GI:4284342
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Life Technologies catalog #: 11548-013
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2143928"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Pan1"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.72 kb. Life Technologies catalog #:
                     11548-013"
ORIGIN

  Query Match             0.7%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   78.3%;  Pred. No. 1e+08;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        726 CGAGACGGTAGAGGGTGAGAAAC 748
```

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                | ||||||||||| |  |||||
Db         23 CAAGACGGTAGAGTCTATGAAAC 1


RESULT 41
AZ595024
LOCUS       AZ595024                  25 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0407D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0407D23 F, genomic survey sequence.
ACCESSION   AZ595024
VERSION     AZ595024.1  GI:11717214
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0407  row: D  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0407D23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             0.7%;  Score 15;  DB 8;  Length 25;
  Best Local Similarity   78.3%;  Pred. No. 1e+08;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2078 CCTGGGTGCTTGTCTGCACAGAG 2100
```

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                  ||  ||| | |||||| ||||||
Db          2 CCCTGGTTCCTGTCTGTACAGAG 24


RESULT 42
AJ587447/c
LOCUS       AJ587447                  25 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            278F11, genomic survey sequence.
ACCESSION   AJ587447
VERSION     AJ587447.1  GI:37937071
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 25)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="278F11"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .25
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match             0.7%;  Score 15;  DB 9;  Length 25;
  Best Local Similarity   78.3%;  Pred. No. 1e+08;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        698 CTTGCAGATTCCACGCCATCGGC 720
              |||||| || ||| | ||| |||
Db         24 CTTGCAAATGCCAGGTCATAGGC 2


RESULT 43
CL693166/c
LOCUS       CL693166                  25 bp    DNA     linear   GSS 10-JUL-2004
DEFINITION  PRI0160a_G12_2 - PRI0160a.BR (25) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL693166
VERSION     CL693166.1  GI:50215074
KEYWORDS    GSS.
```

```
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match             0.7%;  Score 15;  DB 9;  Length 25;
  Best Local Similarity   78.3%;  Pred. No. 1e+08;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2157 CCTCTGCTCAGACACTGTGTGGG 2179
              ||||||| |||  | |||| |||
Db         23 CCTCTGCGCAGGTAATGTGCGGG 1


RESULT 44
CG708385/c
LOCUS       CG708385                 27 bp    DNA     linear   GSS 20-OCT-2003
DEFINITION  1119009A09.2EL_x1 1119 - RescueMu Grid AA Zea mays genomic, genomic
            survey sequence.
ACCESSION   CG708385
VERSION     CG708385.1  GI:37734291
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Walbot,V.
  TITLE     Maize genomic sequences found using engineered RescueMu transposon
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Possible ligation site of ends cut by 2 different endonucleases.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1119009  row: A  column: 09
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="mixed background W23/A188/B73/K55"
                     /db_xref="taxon:4577"
                     /tissue_type="leaf"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="1119 - RescueMu Grid AA"
                     /note="Organ: leaf; Vector: RescueMu (engineered from
                     pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
                     RescueMu is a 4.9 kb, modified maize Mu transposon
                     designed to allow plasmid rescue from total genomic DNA.
                     Mu elements insert preferentially into transcription
                     units. For more information on RescueMu, go to the web
                     site 'www.zmdb.iastate.edu' and follow the links for
                     'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
                     was extracted from leaf strips, double digested using
                     BamHI and BglII, and ligated to form circular plasmids.
                     DH10B cells were transformed and then screened on LB
                     plates with ampicillin."
ORIGIN

  Query Match             0.7%;  Score 15;  DB 9;  Length 27;
  Best Local Similarity   78.3%;  Pred. No. 1.1e+08;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        917 TCCTGAACCGGGAGGTGGAGAGG 939
              | ||||| ||||| |||||| |
Db         23 TGCTGAAGCGGGAACTGGAGAAG 1


RESULT 45
AU257198/c
LOCUS       AU257198                 29 bp    mRNA    linear   EST 25-APR-2002
DEFINITION  AU257198 3'-directed mouse cDNA library Mus musculus cDNA clone
            BED0009981 3', mRNA sequence.
ACCESSION   AU257198
VERSION     AU257198.1  GI:20321583
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Kato,K. and Matoba,R.
  TITLE     Generation of expressed sequence tags from mouse brain
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
            Tel: 81-743-72-5581
            Fax: 81-743-72-5589
            Email: kkato@bs.aist-nara.ac.jp,
            URL:http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="BED0009981"
                     /tissue_type="brain"
                     /clone_lib="3'-directed mouse cDNA library"
ORIGIN

  Query Match             0.7%;  Score 15;  DB 1;  Length 29;
  Best Local Similarity   78.3%;  Pred. No. 1.1e+08;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1841 CCTTGCTGTCCTGTGCAGTGAAG 1863
              ||||| |||| || | || ||||
Db         26 CCTTGGTGTCTTGAGAAGAGAAG 4


RESULT 46
CO787079
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LOCUS       CO787079                 29 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  BL288A_F02 6-Day Axolotl Tail Blastema (6DAxBL) Ambystoma mexicanum
            cDNA 5', similar to hypothetical protein, mRNA sequence.
ACCESSION   CO787079
VERSION     CO787079.1  GI:51003059
KEYWORDS    EST.
SOURCE      Ambystoma mexicanum (axolotl)
  ORGANISM  Ambystoma mexicanum
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
            Ambystoma.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
            Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
  TITLE     An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
            expressed sequence tags from embryonic and regenerating blastema
            cDNA libraries
  JOURNAL   Genome Biol. (2004) In press
COMMENT     Contact: Elly M. Tanaka
            Tanaka Lab
            Max Planck Institute of Molecular Cell Biology and Genetics,
            Dresden
            Pfotenhauerstrasse 108,01307 Dresden, Germany
            Tel: 0049 351 210 2620
            Fax: 0049 351 210 1489
            Email: tanaka@mpi-cbg.de
            Plate: BL288A  row: 02  column: F
            Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Ambystoma mexicanum"
                     /mol_type="mRNA"
                     /db_xref="taxon:8296"
                     /tissue_type="Tail Blastema"
                     /cell_type="regenerating tail blastema"
                     /clone_lib="6-Day Axolotl Tail Blastema (6DAxBL)"
                     /note="Vector: pCMVSport6; Site_1: NotI; Site_2: SalI;
                     Unnormalized cDNA plasmid library prepared by Invitrogen.
                     Size fractionated mRNA was polydT primed and cloned into
                     NotI-SalI site of pCMVSport6. Bacterial host is
                     EMDH10B-TONA. Average insert size is 1.67 kB.
                     TAG_LIB=6DAxBL"
ORIGIN

  Query Match             0.7%;  Score 15;  DB 7;  Length 29;
  Best Local Similarity   78.3%;  Pred. No. 1.1e+08;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        543 CCGGCATTGCCGGGCACCCTGCT 565
              |||| ||| ||||| | |||| |
Db          7 CCGGAATTCCCGGGGATCCTGTT 29


RESULT 47
AZ618807
LOCUS       AZ618807                 29 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0450N11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0450N11 R, genomic survey sequence.
ACCESSION   AZ618807
VERSION     AZ618807.1  GI:11740997
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0450  row: N  column: 11
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0450N11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             0.7%;  Score 15;  DB 8;  Length 29;
  Best Local Similarity   78.3%;  Pred. No. 1.1e+08;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1747 TTCAGAGACTGCGGAGGGGCTTG 1769
              | |||||||||| ||||| | | |
Db          2 TACAGAGACTGGGGAGGTGATGG 24


RESULT 48
AZ632209/c
LOCUS       AZ632209                 30 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0486B18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0486B18 R, genomic survey sequence.
ACCESSION   AZ632209
VERSION     AZ632209.1  GI:11754399
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
```

```
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0486  row: B  column: 18
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 30.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0486B18"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match              0.7%;  Score 15;  DB 8;  Length 30;
  Best Local Similarity   78.3%;  Pred. No. 1.1e+08;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2105 GGTCTGTGCCACCTTGGCCAGGC 2127
                ||| |||||||||   ||| |||
Db         24 GGTGTGTGCCACCACTGCCGGGC 2


RESULT 49
BM400727
LOCUS       BM400727                 26 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-78-C05.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM400727
VERSION     BM400727.1  GI:18200780
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES              Location/Qualifiers
     source           1. .26
                      /organism="Tetrahymena thermophila"
                      /mol_type="mRNA"
                      /strain="CU428.1"
                      /db_xref="taxon:5911"
                      /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                      /note="Vector: BlueScript2 SK+; Details on library
                      preparation can be found in Chilcoat and Turkewitz (2001)
                      Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

  Query Match              0.7%;  Score 14.8;  DB 4;  Length 26;
  Best Local Similarity   88.9%;  Pred. No. 1.2e+08;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        832 GACCAGAGCCACGCGGGG 849
              || | ||||||||||||||
Db          5 GAACTGAGCCACGCGGGG 22


RESULT 50
AU008030/c
LOCUS       AU008030                 27 bp    mRNA    linear   EST 31-JUL-1998
DEFINITION  AU008030 Schizosaccharomyces pombe late log phase cDNA
            Schizosaccharomyces pombe cDNA clone spc02785, mRNA sequence.
ACCESSION   AU008030
VERSION     AU008030.1  GI:3344488
KEYWORDS    EST.
SOURCE      Schizosaccharomyces pombe (fission yeast)
  ORGANISM  Schizosaccharomyces pombe
            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
            Schizosaccharomycetales; Schizosaccharomycetaceae;
            Schizosaccharomyces.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Morimyo,M. and Mita,K.
  TITLE     Identification of expressed sequence tags of Schizosaccharomyces
            pombe
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Mitsuoki Morimyo
            Genome Research Group
            National Institute of Radiological Sciences
            9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
            Email: morimyo@nirs.go.jp.
FEATURES              Location/Qualifiers
     source           1. .27
                      /organism="Schizosaccharomyces pombe"
                      /mol_type="mRNA"
                      /strain="972"
                      /db_xref="taxon:4896"
                      /clone="spc02785"
                      /sex="h minus"
                      /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
                      /note="Vector: M13mp19; The cDNA library of
                      Schizosaccharomyces pombe was prepared by cloning cDNA
                      into the SmaI site of M13mp19 DNA and the direction of DNA
                      sequences was not always from 5' to 3'. The cDNA data of
                      Schizosaccharomyces pombe are available for searching on
                      the World Wide Web.  (URL, http://www.nirs.go.jp)"
ORIGIN

  Query Match              0.7%;  Score 14.8;  DB 1;  Length 27;
  Best Local Similarity   73.1%;  Pred. No. 1.2e+08;
  Matches   19;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2234 GACAGAGTTATTAAACCATTACAAAT 2259
              |||||  |||| ||| || |  ||||
Db         26 GACAGGATTATGAAATCAATTAAAAT 1
```

Search completed: November 20, 2004, 09:19:15
Job time : 7062 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 19, 2004, 11:03:31 ; Search time 1077 Seconds
(without alignments)
11025.246 Million cell updates/sec

Title: US-10-067-125-2
Perfect score: 2262
Sequence: 1 gaattccggcgcgctgcgac.....attaaaccattacaaatctc 2262

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3366436

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	26	1.1	27	5	AAD01954	Aad01954 Probe to
c	2	24	1.1	24	12	ADG09448	Adg09448 TNF-alpha
c	3	23	1.0	23	5	AAD01953	Aad01953 3' RT-PCR
c	4	23	1.0	23	5	AAD02074	Aad02074 3' PCR pr
c	5	23	1.0	23	12	ADN35561	Adn35561 Human NSC
	6	23	1.0	23	12	ADN35560	Adn35560 Human NSC
	7	23	1.0	30	2	AAV03321	Aav03321 Forward P
	8	23	1.0	30	4	AAD04330	Aad04330 Human TRA
	9	22.6	1.0	30	12	ADO15273	Ado15273 TRAF2-spe
	10	22	1.0	22	12	ADG09447	Adg09447 TNF-alpha
	11	21	0.9	21	4	AAF96999	Aaf96999 Human gen
	12	21	0.9	21	4	AAH62439	Aah62439 TRAP3 pol
	13	21	0.9	21	5	AAD01950	Aad01950 Human TRA
c	14	20	0.9	20	3	AAA55539	Aaa55539 TRAF2 ant
c	15	20	0.9	20	3	AAA55545	Aaa55545 TRAF2 ant
c	16	20	0.9	20	3	AAA55543	Aaa55543 TRAF2 ant
c	17	20	0.9	20	3	AAA55537	Aaa55537 TRAF2 ant
c	18	20	0.9	20	3	AAA55550	Aaa55550 TRAF2 ant
c	19	20	0.9	20	3	AAA55548	Aaa55548 TRAF2 ant
c	20	20	0.9	20	3	AAA55549	Aaa55549 TRAF2 ant
c	21	20	0.9	20	3	AAA55541	Aaa55541 TRAF2 ant
c	22	20	0.9	20	3	AAA55551	Aaa55551 TRAF2 ant
c	23	20	0.9	20	3	AAA55555	Aaa55555 TRAF2 ant
c	24	20	0.9	20	3	AAA55544	Aaa55544 TRAF2 ant
c	25	20	0.9	20	3	AAA55546	Aaa55546 TRAF2 ant
c	26	20	0.9	20	3	AAA55554	Aaa55554 TRAF2 ant
c	27	20	0.9	20	3	AAA55557	Aaa55557 TRAF2 ant
c	28	20	0.9	20	3	AAA55556	Aaa55556 TRAF2 ant
c	29	20	0.9	20	3	AAA55538	Aaa55538 TRAF2 ant
c	30	20	0.9	20	3	AAA55540	Aaa55540 TRAF2 ant
c	31	20	0.9	20	3	AAA55542	Aaa55542 TRAF2 ant
c	32	20	0.9	20	3	AAA55536	Aaa55536 TRAF2 ant
c	33	20	0.9	20	3	AAA55547	Aaa55547 TRAF2 ant
c	34	20	0.9	20	3	AAA55552	Aaa55552 TRAF2 ant
c	35	20	0.9	20	3	AAA55553	Aaa55553 TRAF2 ant
	36	20	0.9	20	5	AAD01952	Aad01952 5' RT-PCR
c	37	20	0.9	28	2	AAV27181	Aav27181 PCR prime
c	38	19.4	0.9	21	5	AAD01951	Aad01951 Human TRA
	39	19.4	0.9	30	10	ADK82643	Adk82643 LHRH(A) g
	40	19.4	0.9	30	10	ADK82641	Adk82641 LHRH(M) g
	41	19	0.8	19	12	ADM11769	Adm11769 TRAF2 sho
	42	19	0.8	19	12	ADQ62132	Adq62132 Anti-TRAF
	43	19	0.8	19	12	ADQ62133	Adq62133 Anti-TRAF
	44	19	0.8	19	12	ADQ62135	Adq62135 Anti-TRAF
	45	19	0.8	19	12	ADQ62134	Adq62134 Anti-TRAF
c	46	19	0.8	30	3	AAZ89685	Aaz89685 Human ADA
	47	18.8	0.8	30	2	AAT66316	Aat66316 Oligonucl
c	48	18.6	0.8	29	6	ABK50863	Abk50863 Cholera t
	49	18.6	0.8	30	6	ABK70442	Abk70442 In-situ a
	50	18.4	0.8	25	9	ACI67643	Aci67643 Human mic

ALIGNMENTS

RESULT 1
AAD01954
ID AAD01954 standard; DNA; 27 BP.
XX
AC AAD01954;
XX
DT 26-MAR-2001 (first entry)
XX
DE Probe to screen for non-spliced and splice variants of human TRAF2 cDNA.
XX
KW Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
KW TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;
KW TRAF2 truncated-deleted; TRAF2TD; antiinflammatory; probe; vasotropic;
KW antipsoriatic; antirheumatic; antiarthritic; antidiabetic;
KW antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis;
KW rheumatoid arthritis; graft versus host disease; cardiovascular disease;
KW non-insulin dependent diabetes; inflammatory bowel disease; stroke;
KW neurodegenerative disease; cardiant; hybridisation probe; ss.
XX
OS Homo sapiens.
XX
PN WO200066737-A1.
XX
PD 09-NOV-2000.
XX
PF 06-APR-2000; 2000WO-US009178.
XX
PR 30-APR-1999; 99US-0131940P.
XX
PA (AVET) AVENTIS PHARM PROD INC.
XX
PI Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;
XX
DR WPI; 2001-007223/01.
XX
PT New nucleic acid encoding variants of tumor necrosis factor receptor
PT associated factors useful for inhibiting tumor necrosis factor alpha-
PT regulated pathways, and for treating Crohn's disease, psoriasis, and
PT rheumatoid arthritis.

XX
PS Example 1; Page 40; 74pp; English.
XX
CC The present invention relates to variants of tumour necrosis factor (TNF)
CC -receptor associated factor (TRAF2). TRAF2 has two variants, a splice
CC variant referred as "TRAF2 truncated" (TRAF2TR) and an expression
CC construct with enhanced dominant negative properties referred as "TRAF2
CC truncated-deleted" (TRAF2TD). TRAF2 variants are capable of inhibiting
CC TNF alpha signalling pathways and for inhibiting diseases involving over
CC production of TNFalpha, TNFalpha pathologies involving hyperactivation of
CC nuclear factor kappa B (NFkB). The variants are also useful for
CC inhibiting and treating inflammatory processes involving TNFalpha such as
CC Crohn's disease, psoriasis, rheumatoid arthritis, graft versus host
CC disease, non-insulin dependent diabetes, inflammatory bowel disease, and
CC neurodegenerative diseases or cardiovascular disease such as cardiac
CC ischaemia-reperfusion injury following myocardial infarction, coronary
CC artery bypass surgery, cardiac transplantation or ischaemia-reperfusion
CC injury in the central nervous system (CNS) following stroke, the
CC progression and rupture of advanced coronary atherosclerotic plaques,
CC development and progression of congestive heart failure, endothelial cell
CC injury following balloon angioplasty, or apoptotic cell death of
CC myocardial cells. The present sequence is a probe used for recognising
CC both non-spliced and splice variants of TRAF2TR (a splice variant of
CC TRAF2) cDNA
XX
SQ Sequence 27 BP; 8 A; 6 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 26; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 386 GATGCACCTGGAAGGGGACCCTGAAA 411
||||||||||||||||||||||||||
Db 1 GATGCACCTGGAAGGGGACCCTGAAA 26

RESULT 2
ADG09448/c
ID ADG09448 standard; DNA; 24 BP.
XX
AC ADG09448;
XX
DT 26-FEB-2004 (first entry)
XX
DE TNF-alpha-related gene TRAF2 PCR primer SEQ ID NO:16.
XX
KW tumour necrosis factor; TNF; tumour necrosis factor alpha; TNF-alpha;
KW TNF-related gene; TNF-alpha-related gene; cancer; human; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN EP1361433-A2.
XX
PD 12-NOV-2003.
XX
PF 08-APR-2003; 2003EP-00252225.
XX
PR 09-APR-2002; 2002JP-00107126.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Yanai Y, Yamamoto S, Yamamoto K, Ikegami H;
XX
DR WPI; 2004-055141/06.
XX
PT Estimating therapeutic efficacy of tumor necrosis factor involves
PT evaluating expression level of tumor necrosis factor-related gene in
PT cancer cell.
XX
PS Example 2; SEQ ID NO 16; 56pp; English.
XX
CC The present invention describes a method (M1) for estimating therapeutic
CC efficacy of tumour necrosis factor (TNF). M1 involves evaluating the
CC expression level of a TNF-related gene in a cancer cell. Also described
CC is a kit for estimating the therapeutic efficacy of TNF, which is used in
CC the treatment of cancers. The kit comprises a thermostable DNA polymerase
CC and an oligonucleotide primer comprising a DNA sequence encoding a gene
CC chosen from a protein kinase B (Akt-1) gene, death receptor (DR3) gene,
CC multidrug resistance-associated protein (MRP5) gene, and multidrug
CC resistance-associated protein (MRP6) gene. The present sequence
CC represents a PCR primer which is used in an example from the present
CC invention.
XX
SQ Sequence 24 BP; 8 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.9e+04;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1223 TGTGTCTGCGTATCTACCTGAACG 1246
||||||||||||||||||||||||
Db 24 TGTGTCTGCGTATCTACCTGAACG 1

RESULT 3
AAD01953/c
ID AAD01953 standard; DNA; 23 BP.
XX
AC AAD01953;
XX
DT 26-MAR-2001 (first entry)
XX
DE 3' RT-PCR primer #2 to determine the tissue distribution of TRAF2TR cDNA.
XX
KW Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
KW TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;
KW TRAF2 truncated-deleted; TRAF2TD; antiinflammatory; RT-PCR primer;
KW vasotropic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic;
KW antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis;
KW rheumatoid arthritis; graft versus host disease; cardiovascular disease;
KW non-insulin dependent diabetes; inflammatory bowel disease; stroke;
KW neurodegenerative disease; cardiant; reverse transcription-PCR; ss.
XX
OS Homo sapiens.
XX
PN WO200066737-A1.
XX
PD 09-NOV-2000.
XX
PF 06-APR-2000; 2000WO-US009178.
XX
PR 30-APR-1999; 99US-0131940P.
XX
PA (AVET) AVENTIS PHARM PROD INC.
XX
PI Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;
XX
DR WPI; 2001-007223/01.
XX
PT New nucleic acid encoding variants of tumor necrosis factor receptor
PT associated factors useful for inhibiting tumor necrosis factor alpha-
PT regulated pathways, and for treating Crohn's disease, psoriasis, and
PT rheumatoid arthritis.
XX
PS Example 1; Page 40; 74pp; English.
XX
CC The present invention relates to variants of tumour necrosis factor (TNF)
CC -receptor associated factor (TRAF2). TRAF2 has two variants, a splice
CC variant referred as "TRAF2 truncated" (TRAF2TR) and an expression
CC construct with enhanced dominant negative properties referred as "TRAF2
CC truncated-deleted" (TRAF2TD). TRAF2 variants are capable of inhibiting
CC TNF alpha signalling pathways and for inhibiting diseases involving over
CC production of TNFalpha, TNFalpha pathologies involving hyperactivation of
CC nuclear factor kappa B (NFkB). The variants are also useful for
CC inhibiting and treating inflammatory processes involving TNFalpha such as

CC Crohn's disease, psoriasis, rheumatoid arthritis, graft versus host
CC disease, non-insulin dependent diabetes, inflammatory bowel disease, and
CC neurodegenerative diseases or cardiovascular disease such as cardiac
CC ischaemia-reperfusion injury following myocardial infarction, coronary
CC artery bypass surgery, cardiac transplantation or ischaemia-reperfusion
CC injury in the central nervous system (CNS) following stroke, the
CC progression and rupture of advanced coronary atherosclerotic plaques,
CC development and progression of congestive heart failure, endothelial cell
CC injury following balloon angioplasty, or apoptotic cell death of
CC myocardial cells. The present sequence is a 3' RT-PCR primer #2 for
CC determining the tissue distribution of TRAF2TR (a splice variant of
CC TRAF2) cDNA
XX
SQ Sequence 23 BP; 4 A; 5 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 1.0%; Score 23; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 702 CAGATTCCACGCCATCGGCTGCC 724
||||||||||||||||||||||||
Db 23 CAGATTCCACGCCATCGGCTGCC 1

RESULT 4
AAD02074/c
ID AAD02074 standard; DNA; 23 BP.
XX
AC AAD02074;
XX
DT 26-MAR-2001 (first entry)
XX
DE 3' PCR primer for preparing N-myc fusion construct.
XX
KW Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
KW TNF-receptor associated factor; TRAF2 truncated; TRAF2TR; TRAF2TD;
KW TRAF2 truncated-deleted; antiinflammatory; cardiant; Myc tag; vasotropic;
KW antipsoriatic; antirheumatic; antiarthritic; antidiabetic;
KW antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis;
KW rheumatoid arthritis; graft versus host disease; cardiovascular disease;
KW non-insulin dependent diabetes; inflammatory bowel disease; stroke;
KW neurodegenerative disease; congestive heart failure; PCR primer;
KW myocardial infarction; nuclear factor kappa B; NFkB; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200066737-A1.
XX
PD 09-NOV-2000.
XX
PF 06-APR-2000; 2000WO-US009178.
XX
PR 30-APR-1999; 99US-0131940P.
XX
PA (AVET) AVENTIS PHARM PROD INC.
XX
PI Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;
XX
DR WPI; 2001-007223/01.
XX
PT New nucleic acid encoding variants of tumor necrosis factor receptor
PT associated factors useful for inhibiting tumor necrosis factor alpha-
PT regulated pathways, and for treating Crohn's disease, psoriasis, and
PT rheumatoid arthritis.
XX
PS Example 3; Page 42; 74pp; English.
XX
CC The present invention relates to variants of tumour necrosis factor (TNF)
CC -receptor associated factor (TRAF2). TRAF2 has two variants, a splice
CC variant referred as "TRAF2 truncated" (TRAF2TR) and an expression
CC construct with enhanced dominant negative properties referred as "TRAF2
CC truncated-deleted" (TRAF2TD). TRAF2 variants are capable of inhibiting
CC TNF alpha signalling pathways and for inhibiting diseases involving over
CC production of TNFalpha, TNFalpha pathologies involving hyperactivation of
CC nuclear factor kappa B (NFkB). The variants are also useful for
CC inhibiting and treating inflammatory processes involving TNFalpha such as
CC Crohn's disease, psoriasis, rheumatoid arthritis, graft versus host
CC disease, non-insulin dependent diabetes, inflammatory bowel disease, and
CC neurodegenerative diseases or cardiovascular disease such as cardiac
CC ischaemia-reperfusion injury following myocardial infarction, coronary
CC artery bypass surgery, cardiac transplantation or ischaemia-reperfusion
CC injury in the central nervous system (CNS) following stroke, the
CC progression and rupture of advanced coronary atherosclerotic plaques,
CC development and progression of congestive heart failure, endothelial cell
CC injury following balloon angioplasty, or apoptotic cell death of
CC myocardial cells. The present sequence is a 3' PCR primer for preparing a
CC fusion construct containing N-myc affinity tag as well as truncated and
CC full length TRAF2. N-myc is useful for determining the effect of TRAF2TR
CC on NFkB activation. Truncated as well as full length TRAF2 were
CC constructed with N-Myc affinity tags in a mammalian expression vector
CC (pcDNA3). N-myc fusion constructs were prepared using 5' and 3' PCR
CC primers
XX
SQ Sequence 23 BP; 6 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.0%; Score 23; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1538 TTGTGGACCTGACAGGGCTCTAA 1560
||||||||||||||||||||||||
Db 23 TTGTGGACCTGACAGGGCTCTAA 1

RESULT 5
ADN35561/c
ID ADN35561 standard; DNA; 23 BP.
XX
AC ADN35561;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NSCLC gene semi-quantitative PCR primer reverse primer #120.
XX
KW ss; primer; cytostatic; gene therapy; vaccine;
KW non-small cell lung cancer; NSCLC; diagnosis; cancer; URLC1.
XX
OS Homo sapiens.
XX
PN WO2004031413-A2.
XX
PD 15-APR-2004.
XX
PF 22-SEP-2003; 2003WO-JP012072.
XX
PR 30-SEP-2002; 2002US-0414673P.
PR 28-FEB-2003; 2003US-0451374P.
PR 28-APR-2003; 2003US-0466100P.
XX
PA (ONCO-) ONCOTHERAPY SCI INC.
PA (UYTY) UNIV TOKYO.
XX
PI Nakamura Y, Daigo Y, Nakatsuru S;
XX
DR WPI; 2004-330206/30.
XX
PT Diagnosing, preventing and treating non-small cell lung cancer (NSCLC)
PT comprises determining an expression level of an NSCLC-associated gene in
PT a sample.
XX
PS Disclosure; SEQ ID NO 242; 394pp; English.
XX
CC The invention relates to a method of diagnosing non-small cell lung
CC cancer (NSCLC) or a predisposition to developing NSCLC in a subject by
CC determining the expression level of a NSCLC-associated gene in a

```
CC   biological sample derived from the subject, where an increase or decrease
CC   of the level compared to a normal control level of the gene indicates
CC   that the subject suffers from or is at risk of developing NSCLC. The
CC   method is useful in diagnosing NSCLC or a predisposition to developing
CC   NSCLC in a subject. The compound, polynucleotide and the encoded
CC   polypeptide and composition are useful in treating or preventing NSCLC.
CC   This sequence corresponds to a primer for semi-quantitative PCR
CC   amplification of genes that are differentially expressed in NSCLC cells.
XX
SQ   Sequence 23 BP; 4 A; 5 C; 6 G; 8 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 23;  DB 12;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2222 CCAGCTCACGAAGACAGAGTTAT 2244
              |||||||||||||||||||||||
Db         23 CCAGCTCACGAAGACAGAGTTAT 1


RESULT 6
ADN35560
ID   ADN35560 standard; DNA; 23 BP.
XX
AC   ADN35560;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human NSCLC gene semi-quantitative PCR primer forward primer #120.
XX
KW   ss; primer; cytostatic; gene therapy; vaccine;
KW   non-small cell lung cancer; NSCLC; diagnosis; cancer; URLC1.
XX
OS   Homo sapiens.
XX
PN   WO2004031413-A2.
XX
PD   15-APR-2004.
XX
PF   22-SEP-2003; 2003WO-JP012072.
XX
PR   30-SEP-2002; 2002US-0414673P.
PR   28-FEB-2003; 2003US-0451374P.
PR   28-APR-2003; 2003US-0466100P.
XX
PA   (ONCO-) ONCOTHERAPY SCI INC.
PA   (UYTY ) UNIV TOKYO.
XX
PI   Nakamura Y,  Daigo Y,  Nakatsuru S;
XX
DR   WPI; 2004-330206/30.
XX
PT   Diagnosing, preventing and treating non-small cell lung cancer (NSCLC)
PT   comprises determining an expression level of an NSCLC-associated gene in
PT   a sample.
XX
PS   Disclosure; SEQ ID NO 241; 394pp; English.
XX
CC   The invention relates to a method of diagnosing non-small cell lung
CC   cancer (NSCLC) or a predisposition to developing NSCLC in a subject by
CC   determining the expression level of a NSCLC-associated gene in a
CC   biological sample derived from the subject, where an increase or decrease
CC   of the level compared to a normal control level of the gene indicates
CC   that the subject suffers from or is at risk of developing NSCLC. The
CC   method is useful in diagnosing NSCLC or a predisposition to developing
CC   NSCLC in a subject. The compound, polynucleotide and the encoded
CC   polypeptide and composition are useful in treating or preventing NSCLC.
CC   This sequence corresponds to a primer for semi-quantitative PCR
CC   amplification of genes that are differentially expressed in NSCLC cells.
XX
SQ   Sequence 23 BP; 4 A; 6 C; 6 G; 7 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 23;  DB 12;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1224 GTGTCTGCGTATCTACCTGAACG 1246
              |||||||||||||||||||||||
Db          1 GTGTCTGCGTATCTACCTGAACG 23


RESULT 7
AAV03321
ID   AAV03321 standard; DNA; 30 BP.
XX
AC   AAV03321;
XX
DT   15-APR-1998  (first entry)
XX
DE   Forward PCR primer used to amplify human TRAF2.
XX
KW   Human tumour necrosis factor receptor-associated factor 2; TRAF2;
KW   TRAF-2 binding protein; NF-kappaB activity; NF-kappaB induction;
KW   intracellular signalling activity; acute hepatitis;
KW   autoimmune-induced cell death; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9737016-A1.
XX
PD   09-OCT-1997.
XX
PF   01-APR-1997;   97WO-IL000117.
XX
PR   02-APR-1996;   96IL-00117800.
PR   26-AUG-1996;   96IL-00119133.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Wallach D,  Malinin N,  Boldin M,  Kovalenko A,  Mett I;
XX
DR   WPI; 1997-503101/46.
XX
PT   DNA encoding tumour necrosis factor receptor-associated factor binding
PT   molecule - used for modulation or mediation in cells of the activity of
PT   NF-kB.
XX
PS   Disclosure; Page 50; 127pp; English.
XX
CC   PCR primers AAV03321-22 were used to amplify human tumour necrosis factor
CC   receptor-associated factor 2 (TRAF2) from a HL60 cDNA library. The TRAF2
CC   protein was used to identify proteins capable of binding to it. The TRAF-
CC   2 binding proteins can be used for modulation or mediation in cells of NF
CC   -kappaB activity or any other intracellular signalling activity modulated
CC   or mediated by TRAF2. TRAF-binding proteins are especially used for
CC   prevention or treatment of pathological conditions associated with NF-
CC   kappaB induction, e.g. acute hepatitis, autoimmune-induced cell death,
CC   e.g. death of the beta Langerhans cells or the pancreas that results in
CC   diabetes, the death of cells in graft rejection, the death of
CC   oligodendrocytes in the brain in multiple sclerosis, and AIDS-inhibited T
CC   cell suicide which causes proliferation of the AIDS virus and hence the
CC   AIDS disease. The proteins are also useful for screening of ligands
CC   capable of binding to a protein, which are useful for modulating cellular
CC   activity modulated/mediated by TRAF2
XX
SQ   Sequence 30 BP; 6 A; 9 C; 9 G; 6 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 23;  DB 2;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 CTCATGGCTGCAGCTAGCGTGAC 74
              |||||||||||||||||||||||
Db          8 CTCATGGCTGCAGCTAGCGTGAC 30
```

RESULT 8
AAD04330
ID AAD04330 standard; DNA; 30 BP.
XX
AC AAD04330;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human TRAF2 forward PCR primer for cloning hTRAF2 from HL60 cDNA library.
XX
KW Human; Tumour Necrosis Factor; TNF; TNF Receptor Associated Factor;
KW TRAF2; TRAF2 binding protein; IREN; IkappaB Regulator; IREN-10B; IREN-E;
KW immunosuppressive; nuclear factor-kappaB; NF-kappaB; cytostatic; tumour;
KW AIDS; acquired immune deficiency syndrome; rheumatic disease; apoptosis;
KW autoimmune disease; septic shock; graft-vs-host reaction; inflammation;
KW anorexia; anti-HIV; therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200116314-A1.
XX
PD 08-MAR-2001.
XX
PF 31-AUG-2000; 2000WO-IL000517.
XX
PR 02-SEP-1999; 99IL-00131719.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Wallach D, Malinin N, Sinha I, Leu S;
XX
DR WPI; 2001-281387/29.
XX
PT New DNA sequence encoding Tumor Necrosis Factor receptor associated
PT factor (TRAF) binding proteins (IREN) for treatment or prevention of
PT pathological conditions associated with NF-kappaB induction.
XX
PS Example; Page 51; 118pp; English.
XX
CC The present DNA sequence is forward PCR primer which is used for cloning
CC human tumour necrosis factor (TNF) receptor-associated factor (hTRAF2)
CC coding sequence from HL60 cDNA library. This primer corresponds to the
CC coding sequence of hTRAF2 starting from the start codon and including a
CC linker with BamHI site. The invention relates to human tumour necrosis
CC factor (TNF) receptor- associated factor (TRAF2) binding protein
CC designated as IREN (IkappaB REgulator), its isoforms IREN-10B, IREN-E and
CC their corresponding cDNA molecules. IREN is useful for
CC modulating/mediating the activity of transcription factor NF (Nuclear
CC Factor)-kappaB or any other intracellular signalling activity mediated by
CC TRAF2. IREN is useful in the prevention and treatment of a pathological
CC condition associated with NF-kappaB induction (abnormal) e.g. AIDS
CC (acquired immune deficiency syndrome), autoimmune diseases, tumours,
CC rheumatic diseases, anorexia, septic shock and graft-vs-host reactions.
CC IREN also plays an important role in the control of inflammation and
CC other non-apoptotic effects of TNF as well as in the control of
CC apoptosis. The invention also relates to method for screening,
CC identifying and producing a molecule capable of modulating activities
CC mediated by IREN. IREN antibodies are useful for the purification of new
CC proteins from different sources, including cell extracts or transformed
CC cell lines, in addition IREN can be used in diagnostic purposes for
CC identifying disorders related to abnormal functioning of cellular effects
CC mediated directly by TRAF proteins
XX
SQ Sequence 30 BP; 6 A; 9 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 1.0%; Score 23; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 CTCATGGCTGCAGCTAGCGTGAC 74
||||||||||||||||||||||||
Db 8 CTCATGGCTGCAGCTAGCGTGAC 30

RESULT 9
ADO15273
ID ADO15273 standard; DNA; 30 BP.
XX
AC ADO15273;
XX
DT 12-AUG-2004 (first entry)
XX
DE TRAF2-specific targeting vector construction related PCR primer SEQ:7.
XX
KW somatic cell gene targeting vector; gene targeting; transfection; PCR;
KW primer; tumour necrosis factor receptor associated factor 2;
KW TNF receptor associated factor 2; TRAF2; TRAF2-specific targeting vector;
KW ss.
XX
OS Synthetic.
XX
PN WO2004042007-A2.
XX
PD 21-MAY-2004.
XX
PF 27-OCT-2003; 2003WO-US033872.
XX
PR 30-OCT-2002; 2002US-0422674P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (BISH/) BISHOP G.
PA (HOST/) HOSTAGER B.
XX
PI Bishop G, Hostager B;
XX
DR WPI; 2004-400662/37.
XX
PT New vector for gene targeting and disruption in somatic cells by
PT homologous recombination comprises a gene targeting construct and an
PT expression cassette.
XX
PS Example 1; SEQ ID NO 7; 74pp; English.
XX
CC The present invention describes a somatic cell gene targeting vector
CC which comprises: (a) a gene targeting construct comprising a first
CC cloning site operably linked to a DNA encoding a positive selection
CC marker, a second cloning site and a first polyadenylation sequence, where
CC the construct is promoterless; and (b) an expression cassette comprising
CC a promoter operably linked to a DNA encoding a negative selection marker
CC and a second polyadenylation sequence. Also described: (1) disrupting a
CC gene of interest in a somatic cell; (2) an isolated cell prepared by the
CC above method; and (3) a somatic cell comprising the above vector. The
CC vector and the methods are useful for gene targeting and disruption in
CC somatic cells. The vector and methods allow for the rapid transfection of
CC cells with desired molecules, and so facilitating the ability to test
CC hypotheses and predictions. In addition, the vector and methods target
CC genes specifically and avoid production of additional unknown and desired
CC mutations, a common result when using chemical mutagens to disrupt
CC somatic cell genes. The methods also require much less time and expense
CC than known methods for gene disruption in somatic cells. The present
CC sequence represents a PCR primer used in the construction of a tumour
CC necrosis factor (TNF) receptor associated factor 2 (TRAF2)-specific
CC targeting vector, which is used in an example from the present invention.
XX
SQ Sequence 30 BP; 4 A; 8 C; 8 G; 10 T; 0 U; 0 Other;

Query Match 1.0%; Score 22.6; DB 12; Length 30;
Best Local Similarity 86.2%; Pred. No. 1.5e+05;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 244 TCTGGGCCTCAGAACTGTGCTGCCTGTGT 272
| ||| | ||||||||||||||||||||||
Db 1 TTTGGTACCCAGAACTGTGCTGCCTGTGT 29

RESULT 10

```
ADG09447
ID   ADG09447 standard; DNA; 22 BP.
XX
AC   ADG09447;
XX
DT   26-FEB-2004  (first entry)
XX
DE   TNF-alpha-related gene TRAF2 PCR primer SEQ ID NO:15.
XX
KW   tumour necrosis factor; TNF; tumour necrosis factor alpha; TNF-alpha;
KW   TNF-related gene; TNF-alpha-related gene; cancer; human; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   EP1361433-A2.
XX
PD   12-NOV-2003.
XX
PF   08-APR-2003; 2003EP-00252225.
XX
PR   09-APR-2002; 2002JP-00107126.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI   Yanai Y,  Yamamoto S,  Yamamoto K,  Ikegami H;
XX
DR   WPI; 2004-055141/06.
XX
PT   Estimating therapeutic efficacy of tumor necrosis factor involves
PT   evaluating expression level of tumor necrosis factor-related gene in
PT   cancer cell.
XX
PS   Example 2; SEQ ID NO 15; 56pp; English.
XX
CC   The present invention describes a method (M1) for estimating therapeutic
CC   efficacy of tumour necrosis factor (TNF). M1 involves evaluating the
CC   expression level of a TNF-related gene in a cancer cell. Also described
CC   is a kit for estimating the therapeutic efficacy of TNF, which is used in
CC   the treatment of cancers. The kit comprises a thermostable DNA polymerase
CC   and an oligonucleotide primer comprising a DNA sequence encoding a gene
CC   chosen from a protein kinase B (Akt-1) gene, death receptor (DR3) gene,
CC   multidrug resistance-associated protein (MRP5) gene, and multidrug
CC   resistance-associated protein (MRP6) gene. The present sequence
CC   represents a PCR primer which is used in an example from the present
CC   invention.
XX
SQ   Sequence 22 BP; 5 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 22;  DB 12;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        904 AACATTGTCTGCGTCCTGAACC 925
              ||||||||||||||||||||||
Db          1 AACATTGTCTGCGTCCTGAACC 22


RESULT 11
AAF96999
ID   AAF96999 standard; DNA; 21 BP.
XX
AC   AAF96999;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #1760.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,A)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 165; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
XX
SQ   Sequence 21 BP; 2 A; 9 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 21;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+05;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        434 GCCGCTGCCCGCTCATGCTGA 454
              |||||||||||||||||||||
Db          1 GCCGCTGCCCGCTCATGCTGA 21


RESULT 12
AAH62439
ID   AAH62439 standard; DNA; 21 BP.
XX
AC   AAH62439;
XX
DT   09-SEP-2004  (revised)
DT   12-SEP-2001  (first entry)
XX
DE   TRAP3 polymorphism containing DNA fragment #340.
XX
KW   Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KW   heart disease; paternity testing; forensic science; ds.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   variation       11
```

```
FT                  /*tag=  a
FT                  /standard_name= "single nucleotide polymorphism"
XX
PN   WO200138576-A2.
XX
PD   31-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-US031639.
XX
PR   24-NOV-1999;   99US-0167334P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2001-367705/38.
XX
PT   New nucleic acid segments of the human genome, particularly from genes
PT   including polymorphic sites,for phenotype correlation, forensics,
PT   paternity testing, medicine and genetic analysis.
XX
PS   Claim 1; Page 57; 80pp; English.
XX
CC   DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC   contain single nucleotide polymorphisms (SNPs). A method is included in
CC   the invention for analysing a nucleic acid sample, which consists of
CC   determining the base occupying any one of the polymorphic sites given in
CC   the SNP containing sequences. The nucleotide sequences can be used in the
CC   diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC   diseases, diseases of the cardiovascular system, and infection by
CC   microorganisms. The oligonucleotides are also useful in the manufacture
CC   of a medicament for the treatment or prophylaxis of the diseases, and as
CC   a pharmaceutical. SNP containing oligonucleotides are useful in
CC   applications such as phenotype correlation, forensics, paternity testing,
CC   medicine and genetic analysis
CC
CC   Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
XX
SQ   Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 21;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+05;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        701 GCAGATTCCACGCCATCGGCT 721
              |||||||||||||||||||||
Db          1 GCAGATTCCACGCCATCGGCT 21


RESULT 13
AAD01950
ID   AAD01950 standard; DNA; 21 BP.
XX
AC   AAD01950;
XX
DT   26-MAR-2001  (first entry)
XX
DE   Human TRAF2TR 5' RT-PCR primer #1 used in TRAF2TR cDNA isolation.
XX
KW   Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
KW   TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;
KW   TRAF2 truncated-deleted; TRAF2TD; antiinflammatory; RT-PCR primer;
KW   vasotropic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic;
KW   antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis;
KW   rheumatoid arthritis; graft versus host disease; cardiovascular disease;
KW   non-insulin dependent diabetes; inflammatory bowel disease; stroke;
KW   neurodegenerative disease; cardiant; reverse transcription-PCR; ss.
XX
OS   Homo sapiens.
XX
PN   WO200066737-A1.
XX
PD   09-NOV-2000.
XX
PF   06-APR-2000; 2000WO-US009178.
XX
PR   30-APR-1999;   99US-0131940P.
XX
PA   (AVET ) AVENTIS PHARM PROD INC.
XX
PI   Searfoss GH,  Pagnoni MF,  Ivashchenko YD,  Guo K,  Clark KL;
XX
DR   WPI; 2001-007223/01.
XX
PT   New nucleic acid encoding variants of tumor necrosis factor receptor
PT   associated factors useful for inhibiting tumor necrosis factor alpha-
PT   regulated pathways, and for treating Crohn's disease, psoriasis, and
PT   rheumatoid arthritis.
XX
PS   Example 1; Page 40; 74pp; English.
XX
CC   The present invention relates to variants of tumour necrosis factor (TNF)
CC   -receptor associated factor (TRAF2). TRAF2 has two variants, a splice
CC   variant referred as "TRAF2 truncated" (TRAF2TR) and an expression
CC   construct with enhanced dominant negative properties referred as "TRAF2
CC   truncated-deleted" (TRAF2TD). TRAF2 variants are capable of inhibiting
CC   TNF alpha signalling pathways and for inhibiting diseases involving over
CC   production of TNFalpha, TNFalpha pathologies involving hyperactivation of
CC   nuclear factor kappa B (NFkB). The variants are also useful for
CC   inhibiting and treating inflammatory processes involving TNFalpha such as
CC   Crohn's disease, psoriasis, rheumatoid arthritis, graft versus host
CC   disease, non-insulin dependent diabetes, inflammatory bowel disease, and
CC   neurodegenerative diseases or cardiovascular disease such as cardiac
CC   ischaemia-reperfusion injury following myocardial infarction, coronary
CC   artery bypass surgery, cardiac transplantation or ischaemia-reperfusion
CC   injury in the central nervous system (CNS) following stroke, the
CC   progression and rupture of advanced coronary atherosclerotic plaques,
CC   development and progression of congestive heart failure, endothelial cell
CC   injury following balloon angioplasty, or apoptotic cell death of
CC   myocardial cells. The present sequence is a 5' RT-PCR primer #1 for
CC   isolating cDNA encoding TRAF2TR (a splice variant of TRAF2)
XX
SQ   Sequence 21 BP; 4 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 21;  DB 5;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+05;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         55 ATGGCTGCAGCTAGCGTGACC 75
              |||||||||||||||||||||
Db          1 ATGGCTGCAGCTAGCGTGACC 21


RESULT 14
AAA55539/c
ID   AAA55539 standard; DNA; 20 BP.
XX
AC   AAA55539;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF2 antisense oligonucleotide ISIS# 16830.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
KW   antisense oligonucleotide; phosphorothioate; antiproliferative;
KW   anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS   Synthetic.
XX
PN   WO200020435-A1.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999;   99WO-US023171.
XX
PR   06-OCT-1998;   98US-00167109.
```

```
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Cowsert LM,  Monia BP,  Xu XS;
XX
DR   WPI; 2000-303732/26.
XX
PT   Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT   necrosis factor receptor-associated factor (TRAF), useful for treating
PT   diseases associated with TRAF expression such as inflammatory diseases.
XX
PS   Example 16; Page 51; 170pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (see AAA55496
CC   -A55757) which are targeted to nucleic acids encoding a human tumour
CC   necrosis factor receptor-associated factor (TRAF). The antisense
CC   sequences comprise at least one modified internucleotide linkage, which
CC   is a phosphorothioate linkage. The oligonucleotides also include at least
CC   one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC   Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC   TRAF1-6. Included in the invention is a method for treating a human
CC   having a disease associated with the expression of TRAF comprising
CC   administering an antisense oligonucleotide. The reduction of jun kinase
CC   activation in cells comprises contacting the cells with an antisense
CC   oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC   selectin expression in cells or tissues comprises contacting the cells or
CC   tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC   The antisense oligonucleotides have antiproliferative and anti-
CC   inflammatory activity and are useful for treating disorders associated
CC   with cell proliferation and inflammation. The antisense oligonucleotides
CC   may also be used as a diagnostic probe for studying gene function
XX
SQ   Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 CTCATGGCTGCAGCTAGCGT 71
              ||||||||||||||||||||
Db         20 CTCATGGCTGCAGCTAGCGT 1


RESULT 15
AAA55545/c
ID   AAA55545 standard; DNA; 20 BP.
XX
AC   AAA55545;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF2 antisense oligonucleotide ISIS# 16836.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
KW   antisense oligonucleotide; phosphorothioate; antiproliferative;
KW   anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS   Synthetic.
XX
PN   WO200020435-A1.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999;   99WO-US023171.
XX
PR   06-OCT-1998;   98US-00167109.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Cowsert LM,  Monia BP,  Xu XS;
XX
DR   WPI; 2000-303732/26.
XX
PT   Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT   necrosis factor receptor-associated factor (TRAF), useful for treating
PT   diseases associated with TRAF expression such as inflammatory diseases.
XX
PS   Example 16; Page 51; 170pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (see AAA55496
CC   -A55757) which are targeted to nucleic acids encoding a human tumour
CC   necrosis factor receptor-associated factor (TRAF). The antisense
CC   sequences comprise at least one modified internucleotide linkage, which
CC   is a phosphorothioate linkage. The oligonucleotides also include at least
CC   one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC   Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC   TRAF1-6. Included in the invention is a method for treating a human
CC   having a disease associated with the expression of TRAF comprising
CC   administering an antisense oligonucleotide. The reduction of jun kinase
CC   activation in cells comprises contacting the cells with an antisense
CC   oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC   selectin expression in cells or tissues comprises contacting the cells or
CC   tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC   The antisense oligonucleotides have antiproliferative and anti-
CC   inflammatory activity and are useful for treating disorders associated
CC   with cell proliferation and inflammation. The antisense oligonucleotides
CC   may also be used as a diagnostic probe for studying gene function
XX
SQ   Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        751 CAGGAGCACGAGGTGCAGTG 770
              ||||||||||||||||||||
Db         20 CAGGAGCACGAGGTGCAGTG 1


RESULT 16
AAA55543/c
ID   AAA55543 standard; DNA; 20 BP.
XX
AC   AAA55543;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF2 antisense oligonucleotide ISIS# 16834.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
KW   antisense oligonucleotide; phosphorothioate; antiproliferative;
KW   anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS   Synthetic.
XX
PN   WO200020435-A1.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999;   99WO-US023171.
XX
PR   06-OCT-1998;   98US-00167109.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Cowsert LM,  Monia BP,  Xu XS;
XX
DR   WPI; 2000-303732/26.
XX
PT   Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT   necrosis factor receptor-associated factor (TRAF), useful for treating
PT   diseases associated with TRAF expression such as inflammatory diseases.
XX
PS   Example 16; Page 51; 170pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (see AAA55496
```

CC -A55757) which are targeted to nucleic acids encoding a human tumour
CC necrosis factor receptor-associated factor (TRAF). The antisense
CC sequences comprise at least one modified internucleotide linkage, which
CC is a phosphorothioate linkage. The oligonucleotides also include at least
CC one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC TRAF1-6. Included in the invention is a method for treating a human
CC having a disease associated with the expression of TRAF comprising
CC administering an antisense oligonucleotide. The reduction of jun kinase
CC activation in cells comprises contacting the cells with an antisense
CC oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC selectin expression in cells or tissues comprises contacting the cells or
CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC The antisense oligonucleotides have antiproliferative and anti-
CC inflammatory activity and are useful for treating disorders associated
CC with cell proliferation and inflammation. The antisense oligonucleotides
CC may also be used as a diagnostic probe for studying gene function
XX
SQ Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 576 CGTGAAGGCGCACCACGAGG 595
||||||||||||||||||||
Db 20 CGTGAAGGCGCACCACGAGG 1

RESULT 17
AAA55537/c
ID AAA55537 standard; DNA; 20 BP.
XX
AC AAA55537;
XX
DT 30-AUG-2000 (first entry)
XX
DE TRAF2 antisense oligonucleotide ISIS# 16828.
XX
KW Tumour necrosis factor receptor-associated factor; TRAF; human;
KW antisense oligonucleotide; phosphorothioate; antiproliferative;
KW anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS Synthetic.
XX
PN WO200020435-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023171.
XX
PR 06-OCT-1998; 98US-00167109.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM, Monia BP, Xu XS;
XX
DR WPI; 2000-303732/26.
XX
PT Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT necrosis factor receptor-associated factor (TRAF), useful for treating
PT diseases associated with TRAF expression such as inflammatory diseases.
XX
PS Example 16; Page 51; 170pp; English.
XX
CC The present invention relates to antisense oligonucleotides (see AAA55496
CC -A55757) which are targeted to nucleic acids encoding a human tumour
CC necrosis factor receptor-associated factor (TRAF). The antisense
CC sequences comprise at least one modified internucleotide linkage, which
CC is a phosphorothioate linkage. The oligonucleotides also include at least
CC one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC TRAF1-6. Included in the invention is a method for treating a human
CC having a disease associated with the expression of TRAF comprising
CC administering an antisense oligonucleotide. The reduction of jun kinase
CC activation in cells comprises contacting the cells with an antisense
CC oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC selectin expression in cells or tissues comprises contacting the cells or
CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC The antisense oligonucleotides have antiproliferative and anti-
CC inflammatory activity and are useful for treating disorders associated
CC with cell proliferation and inflammation. The antisense oligonucleotides
CC may also be used as a diagnostic probe for studying gene function
XX
SQ Sequence 20 BP; 3 A; 9 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CGGCGCGCTGCGACCGTTGG 26
||||||||||||||||||||
Db 20 CGGCGCGCTGCGACCGTTGG 1

RESULT 18
AAA55550/c
ID AAA55550 standard; DNA; 20 BP.
XX
AC AAA55550;
XX
DT 30-AUG-2000 (first entry)
XX
DE TRAF2 antisense oligonucleotide ISIS# 16841.
XX
KW Tumour necrosis factor receptor-associated factor; TRAF; human;
KW antisense oligonucleotide; phosphorothioate; antiproliferative;
KW anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS Synthetic.
XX
PN WO200020435-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023171.
XX
PR 06-OCT-1998; 98US-00167109.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM, Monia BP, Xu XS;
XX
DR WPI; 2000-303732/26.
XX
PT Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT necrosis factor receptor-associated factor (TRAF), useful for treating
PT diseases associated with TRAF expression such as inflammatory diseases.
XX
PS Example 16; Page 52; 170pp; English.
XX
CC The present invention relates to antisense oligonucleotides (see AAA55496
CC -A55757) which are targeted to nucleic acids encoding a human tumour
CC necrosis factor receptor-associated factor (TRAF). The antisense
CC sequences comprise at least one modified internucleotide linkage, which
CC is a phosphorothioate linkage. The oligonucleotides also include at least
CC one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC TRAF1-6. Included in the invention is a method for treating a human
CC having a disease associated with the expression of TRAF comprising
CC administering an antisense oligonucleotide. The reduction of jun kinase
CC activation in cells comprises contacting the cells with an antisense
CC oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC selectin expression in cells or tissues comprises contacting the cells or
CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC The antisense oligonucleotides have antiproliferative and anti-

```
CC   inflammatory activity and are useful for treating disorders associated
CC   with cell proliferation and inflammation. The antisense oligonucleotides
CC   may also be used as a diagnostic probe for studying gene function
XX
SQ   Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1533 GGCCATTGTGGACCTGACAG 1552
              ||||||||||||||||||||
Db         20 GGCCATTGTGGACCTGACAG 1


RESULT 19
AAA55548/c
ID   AAA55548 standard; DNA; 20 BP.
XX
AC   AAA55548;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF2 antisense oligonucleotide ISIS# 16839.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
KW   antisense oligonucleotide; phosphorothioate; antiproliferative;
KW   anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS   Synthetic.
XX
PN   WO200020435-A1.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999;   99WO-US023171.
XX
PR   06-OCT-1998;   98US-00167109.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Cowsert LM,  Monia BP,  Xu XS;
XX
DR   WPI; 2000-303732/26.
XX
PT   Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT   necrosis factor receptor-associated factor (TRAF), useful for treating
PT   diseases associated with TRAF expression such as inflammatory diseases.
XX
PS   Example 16; Page 51; 170pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (see AAA55496
CC   -A55757) which are targeted to nucleic acids encoding a human tumour
CC   necrosis factor receptor-associated factor (TRAF). The antisense
CC   sequences comprise at least one modified internucleotide linkage, which
CC   is a phosphorothioate linkage. The oligonucleotides also include at least
CC   one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC   Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC   TRAF1-6. Included in the invention is a method for treating a human
CC   having a disease associated with the expression of TRAF comprising
CC   administering an antisense oligonucleotide. The reduction of jun kinase
CC   activation in cells comprises contacting the cells with an antisense
CC   oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC   selectin expression in cells or tissues comprises contacting the cells or
CC   tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC   The antisense oligonucleotides have antiproliferative and anti-
CC   inflammatory activity and are useful for treating disorders associated
CC   with cell proliferation and inflammation. The antisense oligonucleotides
CC   may also be used as a diagnostic probe for studying gene function
XX
SQ   Sequence 20 BP; 1 A; 8 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1240 CTGAACGGCGACGGCACCGG 1259
              ||||||||||||||||||||
Db         20 CTGAACGGCGACGGCACCGG 1


RESULT 20
AAA55549/c
ID   AAA55549 standard; DNA; 20 BP.
XX
AC   AAA55549;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF2 antisense oligonucleotide ISIS# 16840.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
KW   antisense oligonucleotide; phosphorothioate; antiproliferative;
KW   anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS   Synthetic.
XX
PN   WO200020435-A1.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999;   99WO-US023171.
XX
PR   06-OCT-1998;   98US-00167109.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Cowsert LM,  Monia BP,  Xu XS;
XX
DR   WPI; 2000-303732/26.
XX
PT   Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT   necrosis factor receptor-associated factor (TRAF), useful for treating
PT   diseases associated with TRAF expression such as inflammatory diseases.
XX
PS   Example 16; Page 51; 170pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (see AAA55496
CC   -A55757) which are targeted to nucleic acids encoding a human tumour
CC   necrosis factor receptor-associated factor (TRAF). The antisense
CC   sequences comprise at least one modified internucleotide linkage, which
CC   is a phosphorothioate linkage. The oligonucleotides also include at least
CC   one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC   Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC   TRAF1-6. Included in the invention is a method for treating a human
CC   having a disease associated with the expression of TRAF comprising
CC   administering an antisense oligonucleotide. The reduction of jun kinase
CC   activation in cells comprises contacting the cells with an antisense
CC   oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC   selectin expression in cells or tissues comprises contacting the cells or
CC   tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC   The antisense oligonucleotides have antiproliferative and anti-
CC   inflammatory activity and are useful for treating disorders associated
CC   with cell proliferation and inflammation. The antisense oligonucleotides
CC   may also be used as a diagnostic probe for studying gene function
XX
SQ   Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1387 GACGCCTTCAGGCCCGACGT 1406
              ||||||||||||||||||||
Db         20 GACGCCTTCAGGCCCGACGT 1
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RESULT 21
AAA55541/c
ID   AAA55541 standard; DNA; 20 BP.
XX
AC   AAA55541;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF2 antisense oligonucleotide ISIS# 16832.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
KW   antisense oligonucleotide; phosphorothioate; antiproliferative;
KW   anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS   Synthetic.
XX
PN   WO200020435-A1.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999;   99WO-US023171.
XX
PR   06-OCT-1998;   98US-00167109.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Cowsert LM,  Monia BP,  Xu XS;
XX
DR   WPI; 2000-303732/26.
XX
PT   Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT   necrosis factor receptor-associated factor (TRAF), useful for treating
PT   diseases associated with TRAF expression such as inflammatory diseases.
XX
PS   Example 16; Page 51; 170pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (see AAA55496
CC   -A55757) which are targeted to nucleic acids encoding a human tumour
CC   necrosis factor receptor-associated factor (TRAF). The antisense
CC   sequences comprise at least one modified internucleotide linkage, which
CC   is a phosphorothioate linkage. The oligonucleotides also include at least
CC   one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC   Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC   TRAF1-6. Included in the invention is a method for treating a human
CC   having a disease associated with the expression of TRAF comprising
CC   administering an antisense oligonucleotide. The reduction of jun kinase
CC   activation in cells comprises contacting the cells with an antisense
CC   oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC   selectin expression in cells or tissues comprises contacting the cells or
CC   tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC   The antisense oligonucleotides have antiproliferative and anti-
CC   inflammatory activity and are useful for treating disorders associated
CC   with cell proliferation and inflammation. The antisense oligonucleotides
CC   may also be used as a diagnostic probe for studying gene function
XX
SQ   Sequence 20 BP; 2 A; 11 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        348 GGAGGTGGAGAGCCTGCCGG 367
              ||||||||||||||||||||
Db         20 GGAGGTGGAGAGCCTGCCGG 1


RESULT 22
AAA55551/c
ID   AAA55551 standard; DNA; 20 BP.
XX
AC   AAA55551;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF2 antisense oligonucleotide ISIS# 16842.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
KW   antisense oligonucleotide; phosphorothioate; antiproliferative;
KW   anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS   Synthetic.
XX
PN   WO200020435-A1.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999;   99WO-US023171.
XX
PR   06-OCT-1998;   98US-00167109.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Cowsert LM,  Monia BP,  Xu XS;
XX
DR   WPI; 2000-303732/26.
XX
PT   Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT   necrosis factor receptor-associated factor (TRAF), useful for treating
PT   diseases associated with TRAF expression such as inflammatory diseases.
XX
PS   Example 16; Page 52; 170pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (see AAA55496
CC   -A55757) which are targeted to nucleic acids encoding a human tumour
CC   necrosis factor receptor-associated factor (TRAF). The antisense
CC   sequences comprise at least one modified internucleotide linkage, which
CC   is a phosphorothioate linkage. The oligonucleotides also include at least
CC   one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC   Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC   TRAF1-6. Included in the invention is a method for treating a human
CC   having a disease associated with the expression of TRAF comprising
CC   administering an antisense oligonucleotide. The reduction of jun kinase
CC   activation in cells comprises contacting the cells with an antisense
CC   oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC   selectin expression in cells or tissues comprises contacting the cells or
CC   tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC   The antisense oligonucleotides have antiproliferative and anti-
CC   inflammatory activity and are useful for treating disorders associated
CC   with cell proliferation and inflammation. The antisense oligonucleotides
CC   may also be used as a diagnostic probe for studying gene function
XX
SQ   Sequence 20 BP; 0 A; 8 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1590 GGCAGCCAGGCACAGCCGGC 1609
              ||||||||||||||||||||
Db         20 GGCAGCCAGGCACAGCCGGC 1


RESULT 23
AAA55555/c
ID   AAA55555 standard; DNA; 20 BP.
XX
AC   AAA55555;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF2 antisense oligonucleotide ISIS# 16846.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
KW   antisense oligonucleotide; phosphorothioate; antiproliferative;
KW   anti-inflammatory; E-selectin; jun kinase; ss.
```

XX
OS Synthetic.
XX
PN WO200020435-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023171.
XX
PR 06-OCT-1998; 98US-00167109.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM, Monia BP, Xu XS;
XX
DR WPI; 2000-303732/26.
XX
PT Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT necrosis factor receptor-associated factor (TRAF), useful for treating
PT diseases associated with TRAF expression such as inflammatory diseases.
XX
PS Example 16; Page 52; 170pp; English.
XX
CC The present invention relates to antisense oligonucleotides (see AAA55496
CC -A55757) which are targeted to nucleic acids encoding a human tumour
CC necrosis factor receptor-associated factor (TRAF). The antisense
CC sequences comprise at least one modified internucleotide linkage, which
CC is a phosphorothioate linkage. The oligonucleotides also include at least
CC one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
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CC TRAF1-6. Included in the invention is a method for treating a human
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CC oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC selectin expression in cells or tissues comprises contacting the cells or
CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC The antisense oligonucleotides have antiproliferative and anti-
CC inflammatory activity and are useful for treating disorders associated
CC with cell proliferation and inflammation. The antisense oligonucleotides
CC may also be used as a diagnostic probe for studying gene function
XX
SQ Sequence 20 BP; 3 A; 7 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1994 GGCCTCCTGCTGGCCAGAGC 2013
||||||||||||||||||||
Db 20 GGCCTCCTGCTGGCCAGAGC 1

RESULT 24
AAA55544/c
ID AAA55544 standard; DNA; 20 BP.
XX
AC AAA55544;
XX
DT 30-AUG-2000 (first entry)
XX
DE TRAF2 antisense oligonucleotide ISIS# 16835.
XX
KW Tumour necrosis factor receptor-associated factor; TRAF; human;
KW antisense oligonucleotide; phosphorothioate; antiproliferative;
KW anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS Synthetic.
XX
PN WO200020435-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023171.
XX
PR 06-OCT-1998; 98US-00167109.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM, Monia BP, Xu XS;
XX
DR WPI; 2000-303732/26.
XX
PT Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT necrosis factor receptor-associated factor (TRAF), useful for treating
PT diseases associated with TRAF expression such as inflammatory diseases.
XX
PS Example 16; Page 51; 170pp; English.
XX
CC The present invention relates to antisense oligonucleotides (see AAA55496
CC -A55757) which are targeted to nucleic acids encoding a human tumour
CC necrosis factor receptor-associated factor (TRAF). The antisense
CC sequences comprise at least one modified internucleotide linkage, which
CC is a phosphorothioate linkage. The oligonucleotides also include at least
CC one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC TRAF1-6. Included in the invention is a method for treating a human
CC having a disease associated with the expression of TRAF comprising
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CC oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC selectin expression in cells or tissues comprises contacting the cells or
CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC The antisense oligonucleotides have antiproliferative and anti-
CC inflammatory activity and are useful for treating disorders associated
CC with cell proliferation and inflammation. The antisense oligonucleotides
CC may also be used as a diagnostic probe for studying gene function
XX
SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 675 GACTTGTGGCAAGTGTCGAG 694
||||||||||||||||||||
Db 20 GACTTGTGGCAAGTGTCGAG 1

RESULT 25
AAA55546/c
ID AAA55546 standard; DNA; 20 BP.
XX
AC AAA55546;
XX
DT 30-AUG-2000 (first entry)
XX
DE TRAF2 antisense oligonucleotide ISIS# 16837.
XX
KW Tumour necrosis factor receptor-associated factor; TRAF; human;
KW antisense oligonucleotide; phosphorothioate; antiproliferative;
KW anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS Synthetic.
XX
PN WO200020435-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023171.
XX
PR 06-OCT-1998; 98US-00167109.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM, Monia BP, Xu XS;

XX
DR WPI; 2000-303732/26.
XX
PT Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT necrosis factor receptor-associated factor (TRAF), useful for treating
PT diseases associated with TRAF expression such as inflammatory diseases.
XX
PS Example 16; Page 51; 170pp; English.
XX
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CC necrosis factor receptor-associated factor (TRAF). The antisense
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CC TRAF1-6. Included in the invention is a method for treating a human
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CC The antisense oligonucleotides have antiproliferative and anti-
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CC with cell proliferation and inflammation. The antisense oligonucleotides
CC may also be used as a diagnostic probe for studying gene function
XX
SQ Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 848 GGTCAGAGCTCCTGCAGAGG 867
||||||||||||||||||||
Db 20 GGTCAGAGCTCCTGCAGAGG 1

RESULT 26
AAA55554/c
ID AAA55554 standard; DNA; 20 BP.
XX
AC AAA55554;
XX
DT 30-AUG-2000 (first entry)
XX
DE TRAF2 antisense oligonucleotide ISIS# 16845.
XX
KW Tumour necrosis factor receptor-associated factor; TRAF; human;
KW antisense oligonucleotide; phosphorothioate; antiproliferative;
KW anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS Synthetic.
XX
PN WO200020435-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023171.
XX
PR 06-OCT-1998; 98US-00167109.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM, Monia BP, Xu XS;
XX
DR WPI; 2000-303732/26.
XX
PT Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT necrosis factor receptor-associated factor (TRAF), useful for treating
PT diseases associated with TRAF expression such as inflammatory diseases.
XX
PS Example 16; Page 52; 170pp; English.
XX
CC The present invention relates to antisense oligonucleotides (see AAA55496
CC -A55757) which are targeted to nucleic acids encoding a human tumour
CC necrosis factor receptor-associated factor (TRAF). The antisense
CC sequences comprise at least one modified internucleotide linkage, which
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CC Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC TRAF1-6. Included in the invention is a method for treating a human
CC having a disease associated with the expression of TRAF comprising
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CC activation in cells comprises contacting the cells with an antisense
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CC selectin expression in cells or tissues comprises contacting the cells or
CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC The antisense oligonucleotides have antiproliferative and anti-
CC inflammatory activity and are useful for treating disorders associated
CC with cell proliferation and inflammation. The antisense oligonucleotides
CC may also be used as a diagnostic probe for studying gene function
XX
SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1916 CCATGTAGCAGGAGCACAGT 1935
||||||||||||||||||||
Db 20 CCATGTAGCAGGAGCACAGT 1

RESULT 27
AAA55557/c
ID AAA55557 standard; DNA; 20 BP.
XX
AC AAA55557;
XX
DT 30-AUG-2000 (first entry)
XX
DE TRAF2 antisense oligonucleotide ISIS# 16848.
XX
KW Tumour necrosis factor receptor-associated factor; TRAF; human;
KW antisense oligonucleotide; phosphorothioate; antiproliferative;
KW anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS Synthetic.
XX
PN WO200020435-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023171.
XX
PR 06-OCT-1998; 98US-00167109.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM, Monia BP, Xu XS;
XX
DR WPI; 2000-303732/26.
XX
PT Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT necrosis factor receptor-associated factor (TRAF), useful for treating
PT diseases associated with TRAF expression such as inflammatory diseases.
XX
PS Example 16; Page 52; 170pp; English.
XX
CC The present invention relates to antisense oligonucleotides (see AAA55496
CC -A55757) which are targeted to nucleic acids encoding a human tumour
CC necrosis factor receptor-associated factor (TRAF). The antisense
CC sequences comprise at least one modified internucleotide linkage, which
CC is a phosphorothioate linkage. The oligonucleotides also include at least

CC one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC TRAF1-6. Included in the invention is a method for treating a human
CC having a disease associated with the expression of TRAF comprising
CC administering an antisense oligonucleotide. The reduction of jun kinase
CC activation in cells comprises contacting the cells with an antisense
CC oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC selectin expression in cells or tissues comprises contacting the cells or
CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC The antisense oligonucleotides have antiproliferative and anti-
CC inflammatory activity and are useful for treating disorders associated
CC with cell proliferation and inflammation. The antisense oligonucleotides
CC may also be used as a diagnostic probe for studying gene function
XX
SQ Sequence 20 BP; 2 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2221 TCCAGCTCACGAAGACAGAG 2240
||||||||||||||||||||
Db 20 TCCAGCTCACGAAGACAGAG 1

RESULT 28
AAA55556/c
ID AAA55556 standard; DNA; 20 BP.
XX
AC AAA55556;
XX
DT 30-AUG-2000 (first entry)
XX
DE TRAF2 antisense oligonucleotide ISIS# 16847.
XX
KW Tumour necrosis factor receptor-associated factor; TRAF; human;
KW antisense oligonucleotide; phosphorothioate; antiproliferative;
KW anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS Synthetic.
XX
PN WO200020435-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023171.
XX
PR 06-OCT-1998; 98US-00167109.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM, Monia BP, Xu XS;
XX
DR WPI; 2000-303732/26.
XX
PT Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT necrosis factor receptor-associated factor (TRAF), useful for treating
PT diseases associated with TRAF expression such as inflammatory diseases.
XX
PS Example 16; Page 52; 170pp; English.
XX
CC The present invention relates to antisense oligonucleotides (see AAA55496
CC -A55757) which are targeted to nucleic acids encoding a human tumour
CC necrosis factor receptor-associated factor (TRAF). The antisense
CC sequences comprise at least one modified internucleotide linkage, which
CC is a phosphorothioate linkage. The oligonucleotides also include at least
CC one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC TRAF1-6. Included in the invention is a method for treating a human
CC having a disease associated with the expression of TRAF comprising
CC administering an antisense oligonucleotide. The reduction of jun kinase
CC activation in cells comprises contacting the cells with an antisense
CC oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC selectin expression in cells or tissues comprises contacting the cells or
CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC The antisense oligonucleotides have antiproliferative and anti-
CC inflammatory activity and are useful for treating disorders associated
CC with cell proliferation and inflammation. The antisense oligonucleotides
CC may also be used as a diagnostic probe for studying gene function
XX
SQ Sequence 20 BP; 5 A; 9 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2117 CTTGGCCAGGCTGGCTGTGG 2136
||||||||||||||||||||
Db 20 CTTGGCCAGGCTGGCTGTGG 1

RESULT 29
AAA55538/c
ID AAA55538 standard; DNA; 20 BP.
XX
AC AAA55538;
XX
DT 30-AUG-2000 (first entry)
XX
DE TRAF2 antisense oligonucleotide ISIS# 16829.
XX
KW Tumour necrosis factor receptor-associated factor; TRAF; human;
KW antisense oligonucleotide; phosphorothioate; antiproliferative;
KW anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS Synthetic.
XX
PN WO200020435-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023171.
XX
PR 06-OCT-1998; 98US-00167109.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM, Monia BP, Xu XS;
XX
DR WPI; 2000-303732/26.
XX
PT Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT necrosis factor receptor-associated factor (TRAF), useful for treating
PT diseases associated with TRAF expression such as inflammatory diseases.
XX
PS Example 16; Page 51; 170pp; English.
XX
CC The present invention relates to antisense oligonucleotides (see AAA55496
CC -A55757) which are targeted to nucleic acids encoding a human tumour
CC necrosis factor receptor-associated factor (TRAF). The antisense
CC sequences comprise at least one modified internucleotide linkage, which
CC is a phosphorothioate linkage. The oligonucleotides also include at least
CC one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC TRAF1-6. Included in the invention is a method for treating a human
CC having a disease associated with the expression of TRAF comprising
CC administering an antisense oligonucleotide. The reduction of jun kinase
CC activation in cells comprises contacting the cells with an antisense
CC oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC selectin expression in cells or tissues comprises contacting the cells or
CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC The antisense oligonucleotides have antiproliferative and anti-
CC inflammatory activity and are useful for treating disorders associated
CC with cell proliferation and inflammation. The antisense oligonucleotides
CC may also be used as a diagnostic probe for studying gene function
XX

```
SQ   Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 GGTCACAGCTCTCATGGCTG 61
              ||||||||||||||||||||
Db         20 GGTCACAGCTCTCATGGCTG 1


RESULT 30
AAA55540/c
ID   AAA55540 standard; DNA; 20 BP.
XX
AC   AAA55540;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF2 antisense oligonucleotide ISIS# 16831.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
KW   antisense oligonucleotide; phosphorothioate; antiproliferative;
KW   anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS   Synthetic.
XX
PN   WO200020435-A1.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999;   99WO-US023171.
XX
PR   06-OCT-1998;   98US-00167109.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Cowsert LM,  Monia BP,  Xu XS;
XX
DR   WPI; 2000-303732/26.
XX
PT   Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT   necrosis factor receptor-associated factor (TRAF), useful for treating
PT   diseases associated with TRAF expression such as inflammatory diseases.
XX
PS   Example 16; Page 51; 170pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (see AAA55496
CC   -A55757) which are targeted to nucleic acids encoding a human tumour
CC   necrosis factor receptor-associated factor (TRAF). The antisense
CC   sequences comprise at least one modified internucleotide linkage, which
CC   is a phosphorothioate linkage. The oligonucleotides also include at least
CC   one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC   Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC   TRAF1-6. Included in the invention is a method for treating a human
CC   having a disease associated with the expression of TRAF comprising
CC   administering an antisense oligonucleotide. The reduction of jun kinase
CC   activation in cells comprises contacting the cells with an antisense
CC   oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC   selectin expression in cells or tissues comprises contacting the cells or
CC   tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC   The antisense oligonucleotides have antiproliferative and anti-
CC   inflammatory activity and are useful for treating disorders associated
CC   with cell proliferation and inflammation. The antisense oligonucleotides
CC   may also be used as a diagnostic probe for studying gene function
XX
SQ   Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        185 CCTTCCAGGCGCAGTGTGGC 204
              ||||||||||||||||||||
Db         20 CCTTCCAGGCGCAGTGTGGC 1


RESULT 31
AAA55542/c
ID   AAA55542 standard; DNA; 20 BP.
XX
AC   AAA55542;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF2 antisense oligonucleotide ISIS# 16833.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
KW   antisense oligonucleotide; phosphorothioate; antiproliferative;
KW   anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS   Synthetic.
XX
PN   WO200020435-A1.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999;   99WO-US023171.
XX
PR   06-OCT-1998;   98US-00167109.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Cowsert LM,  Monia BP,  Xu XS;
XX
DR   WPI; 2000-303732/26.
XX
PT   Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT   necrosis factor receptor-associated factor (TRAF), useful for treating
PT   diseases associated with TRAF expression such as inflammatory diseases.
XX
PS   Example 16; Page 51; 170pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (see AAA55496
CC   -A55757) which are targeted to nucleic acids encoding a human tumour
CC   necrosis factor receptor-associated factor (TRAF). The antisense
CC   sequences comprise at least one modified internucleotide linkage, which
CC   is a phosphorothioate linkage. The oligonucleotides also include at least
CC   one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC   Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC   TRAF1-6. Included in the invention is a method for treating a human
CC   having a disease associated with the expression of TRAF comprising
CC   administering an antisense oligonucleotide. The reduction of jun kinase
CC   activation in cells comprises contacting the cells with an antisense
CC   oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC   selectin expression in cells or tissues comprises contacting the cells or
CC   tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC   The antisense oligonucleotides have antiproliferative and anti-
CC   inflammatory activity and are useful for treating disorders associated
CC   with cell proliferation and inflammation. The antisense oligonucleotides
CC   may also be used as a diagnostic probe for studying gene function
XX
SQ   Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        422 GCTGCCACGAAGGCCGCTGC 441
              ||||||||||||||||||||
Db         20 GCTGCCACGAAGGCCGCTGC 1


RESULT 32
AAA55536/c
ID   AAA55536 standard; DNA; 20 BP.
```

```
XX
AC   AAA55536;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF2 antisense oligonucleotide ISIS# 16827.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
KW   antisense oligonucleotide; phosphorothioate; antiproliferative;
KW   anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS   Synthetic.
XX
PN   WO200020435-A1.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999;   99WO-US023171.
XX
PR   06-OCT-1998;   98US-00167109.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Cowsert LM,  Monia BP,  Xu XS;
XX
DR   WPI; 2000-303732/26.
XX
PT   Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT   necrosis factor receptor-associated factor (TRAF), useful for treating
PT   diseases associated with TRAF expression such as inflammatory diseases.
XX
PS   Example 16; Page 51; 170pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (see AAA55496
CC   -A55757) which are targeted to nucleic acids encoding a human tumour
CC   necrosis factor receptor-associated factor (TRAF). The antisense
CC   sequences comprise at least one modified internucleotide linkage, which
CC   is a phosphorothioate linkage. The oligonucleotides also include at least
CC   one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC   Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC   TRAF1-6. Included in the invention is a method for treating a human
CC   having a disease associated with the expression of TRAF comprising
CC   administering an antisense oligonucleotide. The reduction of jun kinase
CC   activation in cells comprises contacting the cells with an antisense
CC   oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC   selectin expression in cells or tissues comprises contacting the cells or
CC   tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC   The antisense oligonucleotides have antiproliferative and anti-
CC   inflammatory activity and are useful for treating disorders associated
CC   with cell proliferation and inflammation. The antisense oligonucleotides
CC   may also be used as a diagnostic probe for studying gene function
XX
SQ   Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCCGGCGCGCTGCGAC 20
              ||||||||||||||||||||
Db         20 GAATTCCGGCGCGCTGCGAC 1


RESULT 33
AAA55547/c
ID   AAA55547 standard; DNA; 20 BP.
XX
AC   AAA55547;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF2 antisense oligonucleotide ISIS# 16838.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
KW   antisense oligonucleotide; phosphorothioate; antiproliferative;
KW   anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS   Synthetic.
XX
PN   WO200020435-A1.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999;   99WO-US023171.
XX
PR   06-OCT-1998;   98US-00167109.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Cowsert LM,  Monia BP,  Xu XS;
XX
DR   WPI; 2000-303732/26.
XX
PT   Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT   necrosis factor receptor-associated factor (TRAF), useful for treating
PT   diseases associated with TRAF expression such as inflammatory diseases.
XX
PS   Example 16; Page 51; 170pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (see AAA55496
CC   -A55757) which are targeted to nucleic acids encoding a human tumour
CC   necrosis factor receptor-associated factor (TRAF). The antisense
CC   sequences comprise at least one modified internucleotide linkage, which
CC   is a phosphorothioate linkage. The oligonucleotides also include at least
CC   one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC   Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC   TRAF1-6. Included in the invention is a method for treating a human
CC   having a disease associated with the expression of TRAF comprising
CC   administering an antisense oligonucleotide. The reduction of jun kinase
CC   activation in cells comprises contacting the cells with an antisense
CC   oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC   selectin expression in cells or tissues comprises contacting the cells or
CC   tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC   The antisense oligonucleotides have antiproliferative and anti-
CC   inflammatory activity and are useful for treating disorders associated
CC   with cell proliferation and inflammation. The antisense oligonucleotides
CC   may also be used as a diagnostic probe for studying gene function
XX
SQ   Sequence 20 BP; 1 A; 8 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        962 GCAGCCGGCAGCACCGGCTG 981
              ||||||||||||||||||||
Db         20 GCAGCCGGCAGCACCGGCTG 1


RESULT 34
AAA55552/c
ID   AAA55552 standard; DNA; 20 BP.
XX
AC   AAA55552;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF2 antisense oligonucleotide ISIS# 16843.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
KW   antisense oligonucleotide; phosphorothioate; antiproliferative;
KW   anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS   Synthetic.
XX
PN   WO200020435-A1.
```

XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023171.
XX
PR 06-OCT-1998; 98US-00167109.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM, Monia BP, Xu XS;
XX
DR WPI; 2000-303732/26.
XX
PT Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT necrosis factor receptor-associated factor (TRAF), useful for treating
PT diseases associated with TRAF expression such as inflammatory diseases.
XX
PS Example 16; Page 52; 170pp; English.
XX
CC The present invention relates to antisense oligonucleotides (see AAA55496
CC -A55757) which are targeted to nucleic acids encoding a human tumour
CC necrosis factor receptor-associated factor (TRAF). The antisense
CC sequences comprise at least one modified internucleotide linkage, which
CC is a phosphorothioate linkage. The oligonucleotides also include at least
CC one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC TRAF1-6. Included in the invention is a method for treating a human
CC having a disease associated with the expression of TRAF comprising
CC administering an antisense oligonucleotide. The reduction of jun kinase
CC activation in cells comprises contacting the cells with an antisense
CC oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC selectin expression in cells or tissues comprises contacting the cells or
CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC The antisense oligonucleotides have antiproliferative and anti-
CC inflammatory activity and are useful for treating disorders associated
CC with cell proliferation and inflammation. The antisense oligonucleotides
CC may also be used as a diagnostic probe for studying gene function
XX
SQ Sequence 20 BP; 3 A; 8 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1685 GGTGTCGGCCTGCAGCCAAG 1704
||||||||||||||||||||
Db 20 GGTGTCGGCCTGCAGCCAAG 1

RESULT 35
AAA55553/c
ID AAA55553 standard; DNA; 20 BP.
XX
AC AAA55553;
XX
DT 30-AUG-2000 (first entry)
XX
DE TRAF2 antisense oligonucleotide ISIS# 16844.
XX
KW Tumour necrosis factor receptor-associated factor; TRAF; human;
KW antisense oligonucleotide; phosphorothioate; antiproliferative;
KW anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS Synthetic.
XX
PN WO200020435-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023171.
XX
PR 06-OCT-1998; 98US-00167109.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM, Monia BP, Xu XS;
XX
DR WPI; 2000-303732/26.
XX
PT Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT necrosis factor receptor-associated factor (TRAF), useful for treating
PT diseases associated with TRAF expression such as inflammatory diseases.
XX
PS Example 16; Page 52; 170pp; English.
XX
CC The present invention relates to antisense oligonucleotides (see AAA55496
CC -A55757) which are targeted to nucleic acids encoding a human tumour
CC necrosis factor receptor-associated factor (TRAF). The antisense
CC sequences comprise at least one modified internucleotide linkage, which
CC is a phosphorothioate linkage. The oligonucleotides also include at least
CC one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC TRAF1-6. Included in the invention is a method for treating a human
CC having a disease associated with the expression of TRAF comprising
CC administering an antisense oligonucleotide. The reduction of jun kinase
CC activation in cells comprises contacting the cells with an antisense
CC oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC selectin expression in cells or tissues comprises contacting the cells or
CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC The antisense oligonucleotides have antiproliferative and anti-
CC inflammatory activity and are useful for treating disorders associated
CC with cell proliferation and inflammation. The antisense oligonucleotides
CC may also be used as a diagnostic probe for studying gene function
XX
SQ Sequence 20 BP; 5 A; 10 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1789 GGCTGTGGTGGCATTGGCCG 1808
||||||||||||||||||||
Db 20 GGCTGTGGTGGCATTGGCCG 1

RESULT 36
AAD01952
ID AAD01952 standard; DNA; 20 BP.
XX
AC AAD01952;
XX
DT 26-MAR-2001 (first entry)
XX
DE 5' RT-PCR primer #2 to determine the tissue distribution of TRAF2TR cDNA.
XX
KW Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
KW TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;
KW TRAF2 truncated-deleted; TRAF2TD; antiinflammatory; RT-PCR primer;
KW vasotropic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic;
KW antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis;
KW rheumatoid arthritis; graft versus host disease; cardiovascular disease;
KW non-insulin dependent diabetes; inflammatory bowel disease; stroke;
KW neurodegenerative disease; cardiant; reverse transcription-PCR; ss.
XX
OS Homo sapiens.
XX
PN WO200066737-A1.
XX
PD 09-NOV-2000.
XX
PF 06-APR-2000; 2000WO-US009178.
XX
PR 30-APR-1999; 99US-0131940P.
XX
PA (AVET) AVENTIS PHARM PROD INC.
XX

```
PI   Searfoss GH,  Pagnoni MF,  Ivashchenko YD,  Guo K,  Clark KL;
XX
DR   WPI; 2001-007223/01.
XX
PT   New nucleic acid encoding variants of tumor necrosis factor receptor
PT   associated factors useful for inhibiting tumor necrosis factor alpha-
PT   regulated pathways, and for treating Crohn's disease, psoriasis, and
PT   rheumatoid arthritis.
XX
PS   Example 1; Page 40; 74pp; English.
XX
CC   The present invention relates to variants of tumour necrosis factor (TNF)
CC   -receptor associated factor (TRAF2). TRAF2 has two variants, a splice
CC   variant referred as "TRAF2 truncated" (TRAF2TR) and an expression
CC   construct with enhanced dominant negative properties referred as "TRAF2
CC   truncated-deleted" (TRAF2TD). TRAF2 variants are capable of inhibiting
CC   TNF alpha signalling pathways and for inhibiting diseases involving over
CC   production of TNFalpha, TNFalpha pathologies involving hyperactivation of
CC   nuclear factor kappa B (NFkB). The variants are also useful for
CC   inhibiting and treating inflammatory processes involving TNFalpha such as
CC   Crohn's disease, psoriasis, rheumatoid arthritis, graft versus host
CC   disease, non-insulin dependent diabetes, inflammatory bowel disease, and
CC   neurodegenerative diseases or cardiovascular disease such as cardiac
CC   ischaemia-reperfusion injury following myocardial infarction, coronary
CC   artery bypass surgery, cardiac transplantation or ischaemia-reperfusion
CC   injury in the central nervous system (CNS) following stroke, the
CC   progression and rupture of advanced coronary atherosclerotic plaques,
CC   development and progression of congestive heart failure, endothelial cell
CC   injury following balloon angioplasty, or apoptotic cell death of
CC   myocardial cells. The present sequence is a 5' RT-PCR primer #2 for
CC   determining the tissue distribution of TRAF2TR (a splice variant of
CC   TRAF2) cDNA
XX
SQ   Sequence 20 BP; 2 A; 6 C; 10 G; 2 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 20;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        351 GGTGGAGAGCCTGCCGGCCG 370
              ||||||||||||||||||||
Db          1 GGTGGAGAGCCTGCCGGCCG 20


RESULT 37
AAV27181/c
ID   AAV27181 standard; DNA; 28 BP.
XX
AC   AAV27181;
XX
DT   17-SEP-1998  (first entry)
XX
DE   PCR primer B9 for G-protein coupled receptor coding sequence.
XX
KW   G-protein coupled receptor; gene therapy; abnormality detection;
KW   short form; human; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   EP845529-A2.
XX
PD   03-JUN-1998.
XX
PF   27-OCT-1997;   97EP-00308562.
XX
PR   29-OCT-1996;   96JP-00286823.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Hinuma S,  Fukusumi S,  Kawamata Y;
XX
DR   WPI; 1998-288746/26.
XX
PT   New human G-protein coupled receptor protein - and corresponding DNA,
PT   ligands, antibodies, etc.
XX
PS   Example 1; Page 25; 65pp; English.
XX
CC   This sequence represents a PCR primer used to isolate DNA encoding a
CC   human G-protein coupled receptor of the invention. The protein or cells
CC   expressing the DNA encoding it can be used to screen for agonists or
CC   antagonists of the receptor, which can be used as drugs for treating
CC   various diseases (none disclosed). The DNA can also be used for practice
CC   drug design based on comparisons with structurally analogous ligands and
CC   receptors. DNA encoding the protein can be used for gene therapy for
CC   diseases caused by a deficiency of the receptor. The DNA can also be used
CC   to detect abnormalities in the gene encoding the receptor. The protein or
CC   fragment can be used to determine levels of receptor ligands in vivo. The
CC   antibody can be used in assays to detect the protein
XX
SQ   Sequence 28 BP; 10 A; 3 C; 13 G; 2 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 20;  DB 2;  Length 28;
  Best Local Similarity   82.1%;  Pred. No. 5.9e+05;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        213 CTGCTCCTTCTGCCTGGCCAGCATCCTC 240
              ||||| |||||||||| ||| | || ||
Db         28 CTGCTACTTCTGCCTGCCCATCCTCTTC 1


RESULT 38
AAD01951/c
ID   AAD01951 standard; DNA; 21 BP.
XX
AC   AAD01951;
XX
DT   26-MAR-2001  (first entry)
XX
DE   Human TRAF2TR 3' RT-PCR primer #1 used in TRAF2TR cDNA isolation.
XX
KW   Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
KW   TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;
KW   TRAF2 truncated-deleted; TRAF2TD; antiinflammatory; RT-PCR primer;
KW   vasotropic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic;
KW   antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis;
KW   rheumatoid arthritis; graft versus host disease; cardiovascular disease;
KW   non-insulin dependent diabetes; inflammatory bowel disease; stroke;
KW   neurodegenerative disease; cardiant; reverse transcription-PCR; ss.
XX
OS   Homo sapiens.
XX
PN   WO200066737-A1.
XX
PD   09-NOV-2000.
XX
PF   06-APR-2000; 2000WO-US009178.
XX
PR   30-APR-1999;   99US-0131940P.
XX
PA   (AVET ) AVENTIS PHARM PROD INC.
XX
PI   Searfoss GH,  Pagnoni MF,  Ivashchenko YD,  Guo K,  Clark KL;
XX
DR   WPI; 2001-007223/01.
XX
PT   New nucleic acid encoding variants of tumor necrosis factor receptor
PT   associated factors useful for inhibiting tumor necrosis factor alpha-
PT   regulated pathways, and for treating Crohn's disease, psoriasis, and
PT   rheumatoid arthritis.
XX
PS   Example 1; Page 40; 74pp; English.
XX
CC   The present invention relates to variants of tumour necrosis factor (TNF)
CC   -receptor associated factor (TRAF2). TRAF2 has two variants, a splice
```

CC variant referred as "TRAF2 truncated" (TRAF2TR) and an expression
CC construct with enhanced dominant negative properties referred as "TRAF2
CC truncated-deleted" (TRAF2TD). TRAF2 variants are capable of inhibiting
CC TNF alpha signalling pathways and for inhibiting diseases involving over
CC production of TNFalpha, TNFalpha pathologies involving hyperactivation of
CC nuclear factor kappa B (NFkB). The variants are also useful for
CC inhibiting and treating inflammatory processes involving TNFalpha such as
CC Crohn's disease, psoriasis, rheumatoid arthritis, graft versus host
CC disease, non-insulin dependent diabetes, inflammatory bowel disease, and
CC neurodegenerative diseases or cardiovascular disease such as cardiac
CC ischaemia-reperfusion injury following myocardial infarction, coronary
CC artery bypass surgery, cardiac transplantation or ischaemia-reperfusion
CC injury in the central nervous system (CNS) following stroke, the
CC progression and rupture of advanced coronary atherosclerotic plaques,
CC development and progression of congestive heart failure, endothelial cell
CC injury following balloon angioplasty, or apoptotic cell death of
CC myocardial cells. The present sequence is a 3' RT-PCR primer #1 used for
CC isolating cDNA encoding TRAF2TR (a splice variant of TRAF2). This 3'
CC primer is also useful for preparing TRAF2TD variant using TRAF2TR cDNA as
CC template
XX
SQ Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.9%; Score 19.4; DB 5; Length 21;
Best Local Similarity 95.2%; Pred. No. 7.5e+05;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1540 GTGGACCTGACAGGGCTCTAA 1560
||||||||||||||||| |||
Db 21 GTGGACCTGACAGGGCTATAA 1

RESULT 39
ADK82643
ID ADK82643 standard; DNA; 30 BP.
XX
AC ADK82643;
XX
DT 06-MAY-2004 (first entry)
XX
DE LHRH(A) gene vaccine construction oligonucleotide L1.
XX
KW ss; gene vaccine; farm animal; castration; LHRH;
KW luteinising hormone releasing hormone; fowl; coliform bacteria.
XX
OS Unidentified.
XX
PN CN1384200-A.
XX
PD 11-DEC-2002.
XX
PF 13-MAR-2002; 2002CN-00103725.
XX
PR 13-MAR-2002; 2002CN-00103725.
XX
PA (DUNN/) DU N.
XX
PI Du N, Li G;
XX
DR WPI; 2003-290678/29.
XX
PT Genetically engineered body of farm animal castration gene vaccine (DNA
PT vaccine).
XX
PS Disclosure; Page 7; 20pp; Chinese.
XX
CC The invention relates to the construction of a gene vaccine for farm
CC animal castration which includes artificial synthesis of livestock-type
CC LHRH(M) gene and fowl-type LHRH(A) gene and construction of pBS-LHRH
CC plasmid; slicing HBs segment from pWR-HBs plasmid and inserting into pBS-
CC LHRH plasmid to constitute pBS-HBs/LHRH plasmid. These are used to
CC convert coliform bacteria to constitute the gene engineering antibody
CC Escherichia coli-pcDNA3.1-HBs/LHRH(M) and E.coli-pcDNA3.1-HBs/LHRH(A).
CC This sequence constitutes an oligonucleotide used to generate the LHRH(A)
CC construct for the gene vaccine.
XX
SQ Sequence 30 BP; 7 A; 8 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 0.9%; Score 19.4; DB 10; Length 30;
Best Local Similarity 79.3%; Pred. No. 8.3e+05;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 232 AGCATCCTCAGCTCTGGGCCTCAGAACTG 260
|| ||||||||| |||| ||| | ||||
Db 2 AGGATCCTCAGCACTGGTCCTATGGACTG 30

RESULT 40
ADK82641
ID ADK82641 standard; DNA; 30 BP.
XX
AC ADK82641;
XX
DT 06-MAY-2004 (first entry)
XX
DE LHRH(M) gene vaccine construction oligonucleotide L1.
XX
KW ss; gene vaccine; farm animal; castration; LHRH;
KW luteinising hormone releasing hormone; fowl; coliform bacteria.
XX
OS Unidentified.
XX
PN CN1384200-A.
XX
PD 11-DEC-2002.
XX
PF 13-MAR-2002; 2002CN-00103725.
XX
PR 13-MAR-2002; 2002CN-00103725.
XX
PA (DUNN/) DU N.
XX
PI Du N, Li G;
XX
DR WPI; 2003-290678/29.
XX
PT Genetically engineered body of farm animal castration gene vaccine (DNA
PT vaccine).
XX
PS Disclosure; Page 7; 20pp; Chinese.
XX
CC The invention relates to the construction of a gene vaccine for farm
CC animal castration which includes artificial synthesis of livestock-type
CC LHRH(M) gene and fowl-type LHRH(A) gene and construction of pBS-LHRH
CC plasmid; slicing HBs segment from pWR-HBs plasmid and inserting into pBS-
CC LHRH plasmid to constitute pBS-HBs/LHRH plasmid. These are used to
CC convert coliform bacteria to constitute the gene engineering antibody
CC Escherichia coli-pcDNA3.1-HBs/LHRH(M) and E.coli-pcDNA3.1-HBs/LHRH(A).
CC This sequence constitutes an oligonucleotide used to generate the LHRH(M)
CC construct for the gene vaccine.
XX
SQ Sequence 30 BP; 7 A; 8 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 0.9%; Score 19.4; DB 10; Length 30;
Best Local Similarity 79.3%; Pred. No. 8.3e+05;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 232 AGCATCCTCAGCTCTGGGCCTCAGAACTG 260
|| ||||||||| |||| ||| | ||||
Db 2 AGGATCCTCAGCACTGGTCCTATGGACTG 30

RESULT 41
ADM11769
ID ADM11769 standard; RNA; 19 BP.
XX

```
AC   ADM11769;
XX
DT   17-JUN-2004  (first entry)
XX
DE   TRAF2 short interfering RNA oligonucleotide sense strand.
XX
KW   antigen presenting cell; short interfering RNA; siRNA; p50 subunit;
KW   NF-kappaB; tumour necrosis factor receptor associated factor 3;
KW   TNF-receptor associated factor 3; c-Rel subunit; NF-kappaB;
KW   immunosuppressive; antiinflammatory; dermatological; antiarthritic;
KW   antirheumatic; neuroprotective; antidiabetic; thyrominetic; muscular;
KW   autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
KW   multiple sclerosis; insulin-dependent diabetes mellitus;
KW   Hashimoto's thyroiditis; myasthenia gravis; ss.
XX
OS   Synthetic.
XX
PN   WO2004027063-A1.
XX
PD   01-APR-2004.
XX
PF   19-SEP-2002; 2002WO-EP012636.
XX
PR   19-SEP-2002; 2002WO-EP012636.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (GENE-) GENETHON III.
PA   (INSR ) INST ROUSSY GUSTAVE.
XX
PI   Galy A,  Laderach D,  Compagno D;
XX
DR   WPI; 2004-295420/27.
XX
PT   Obtaining isolated or cultured antigen presenting cells, useful in
PT   treating or preventing a disease, e.g. autoimmune diseases, comprises
PT   introducing in the cells siRNA directed against the target gene.
XX
PS   Example 2; SEQ ID NO 6; 31pp; English.
XX
CC   The present invention describes a method for obtaining isolated or
CC   cultured antigen presenting cells where the expression of one or more
CC   target gene(s) is down-regulated. The method comprises introducing in the
CC   cells short interfering RNA (siRNA) oligonucleotides directed against the
CC   target gene(s). Also described: (1) a siRNA directed against a target
CC   gene, e.g. a gene encoding the p50 subunit of NF-kappaB, tumour necrosis
CC   factor (TNF)-receptor associated factor 3 or c-Rel subunit of NF-kappaB;
CC   (2) an expression vector containing a DNA template for a siRNA of (1);
CC   (3) a antigen-presenting cell obtainable by the method above; (4) a
CC   method of producing T lymphocytes that fail to produce IFN-gamma; and (5)
CC   a pharmaceutical composition comprising an antigen-presenting cell of (3)
CC   and activated T lymphocytes obtainable by the method of (4). The siRNAs
CC   have immunosuppressive, antiinflammatory, dermatological, antiarthritic,
CC   antirheumatic, neuroprotective, antidiabetic, thyrominetic and muscular
CC   activities. The siRNA or expression vector is useful in preparing an
CC   immunosuppressive therapeutic composition. The method is useful in
CC   obtaining isolated or cultured antigen presenting cells. The method and
CC   composition is useful in treating or preventing a disease, e.g.
CC   autoimmune diseases like systemic lupus erythematosus, rheumatoid
CC   arthritis, multiple sclerosis, insulin-dependent diabetes mellitus,
CC   Hashimoto's thyroiditis or myasthenia gravis. The present sequence
CC   represents an siRNA oligonucleotide which is used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 19 BP; 6 A; 5 C; 6 G; 0 T; 2 U; 0 Other;

  Query Match             0.8%;  Score 19;  DB 12;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 9e+05;
  Matches   17;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        412 GAATACGAGAGCTGCCACG 430
              |||:||||||||:||||||
Db          1 GAAUACGAGAGCUGCCACG 19
```

```
RESULT 42
ADQ62132
ID   ADQ62132 standard; RNA; 19 BP.
XX
AC   ADQ62132;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Anti-TRAF2 siRNA SEQ ID NO:1834.
XX
KW   ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW   RNA interference.
XX
OS   Synthetic.
XX
PN   WO2004045543-A2.
XX
PD   03-JUN-2004.
XX
PF   14-NOV-2003; 2003WO-US036787.
XX
PR   14-NOV-2002; 2002US-0426137P.
PR   10-SEP-2003; 2003US-0502050P.
XX
PA   (DHAR-) DHARMACON INC.
XX
PI   Anastasia K,  Angela R,  Devin L,  William M,  Stephen S;
XX
DR   WPI; 2004-420527/39.
XX
PT   Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
PT   by selecting a target gene and measuring the functionality of the
PT   nucleotide sequences that are complementary to a stretch of nucleotides
PT   of the target sequence.
XX
PS   Example 12; SEQ ID NO 1834; 199pp; English.
XX
CC   The invention relates to a novel method for selecting siRNA (short
CC   interfering RNA) comprising selecting an siRNA molecule of 19-25
CC   nucleoside bases by selecting a target gene and measuring the
CC   functionality of sequences of 19-25 nucleotides in length that are
CC   substantially complementary to a stretch of nucleotides of the target
CC   sequence, where the functionality is dependent upon non-target specific
CC   criteria. Also claimed are methods for gene-silencing, developing an
CC   siRNA algorithm for selecting siRNA, selecting an siRNA with improved
CC   functionality, selecting hyperfunctional siRNA, an siRNA molecule
CC   effective at silencing Bcl-2, and a kit for gene silencing comprising the
CC   siRNA. The siRNA molecule comprises a sequence substantially similar to a
CC   sequence consisting of GGGAGAUAGUGAUGAAGUA; GAAGUACAUCCAUUAUAAG;
CC   GUACGACAACCGGGAGAUA; AGAUAGUGAUGAAGUACAU; UGAAGACUCUGCUCAGUUU;
CC   CAUGCGGCCUCUGUUUGA; UGCGGCCUCUGUUUGAUUU; GAGAUAGUGAUGAAGUACA;
CC   GGAGAUAGUGAUGAAGUAC; and GAAGACUCUGCUCAGUUUG. The siRNA molecule
CC   comprises a sense strand and an anti-sense strand. The siRNA molecule
CC   comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
CC   pairs. The kit comprises at least two siRNA, comprising a first optimised
CC   siRNA and a second optimised siRNA. The method is useful in selecting
CC   siRNA for generating a gene silencing reagent. The present sequence is
CC   used in the exemplification of the invention.
XX
SQ   Sequence 19 BP; 9 A; 2 C; 4 G; 0 T; 4 U; 0 Other;

  Query Match             0.8%;  Score 19;  DB 12;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 9e+05;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2231 GAAGACAGAGTTATTAAAC 2249
              ||||||||||::|::||||
Db          1 GAAGACAGAGUUAUUAAAC 19


RESULT 43
ADQ62133
```

ID ADQ62133 standard; RNA; 19 BP.
XX
AC ADQ62133;
XX
DT 09-SEP-2004 (first entry)
XX
DE Anti-TRAF2 siRNA SEQ ID NO:1835.
XX
KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW RNA interference.
XX
OS Synthetic.
XX
PN WO2004045543-A2.
XX
PD 03-JUN-2004.
XX
PF 14-NOV-2003; 2003WO-US036787.
XX
PR 14-NOV-2002; 2002US-0426137P.
PR 10-SEP-2003; 2003US-0502050P.
XX
PA (DHAR-) DHARMACON INC.
XX
PI Anastasia K, Angela R, Devin L, William M, Stephen S;
XX
DR WPI; 2004-420527/39.
XX
PT Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
PT by selecting a target gene and measuring the functionality of the
PT nucleotide sequences that are complementary to a stretch of nucleotides
PT of the target sequence.
XX
PS Example 12; SEQ ID NO 1835; 199pp; English.
XX
CC The invention relates to a novel method for selecting siRNA (short
CC interfering RNA) comprising selecting an siRNA molecule of 19-25
CC nucleoside bases by selecting a target gene and measuring the
CC functionality of sequences of 19-25 nucleotides in length that are
CC substantially complementary to a stretch of nucleotides of the target
CC sequence, where the functionality is dependent upon non-target specific
CC criteria. Also claimed are methods for gene-silencing, developing an
CC siRNA algorithm for selecting siRNA, selecting an siRNA with improved
CC functionality, selecting hyperfunctional siRNA, an siRNA molecule
CC effective at silencing Bcl-2, and a kit for gene silencing comprising the
CC siRNA. The siRNA molecule comprises a sequence substantially similar to a
CC sequence consisting of GGGAGAUAGUGAUGAAGUA; GAAGUACAUCCAUUAUAAG;
CC GUACGACAACCGGGAGAUA; AGAUAGUGAUGAAGUACAU; UGAAGACUCUGCUCAGUUU;
CC CAUGCGGCCUCUGUUUGA; UGCGGCCUCUGUUUGAUUU; GAGAUAGUGAUGAAGUACA;
CC GGAGAUAGUGAUGAAGUAC; and GAAGACUCUGCUCAGUUUG. The siRNA molecule
CC comprises a sense strand and an anti-sense strand. The siRNA molecule
CC comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
CC pairs. The kit comprises at least two siRNA, comprising a first optimised
CC siRNA and a second optimised siRNA. The method is useful in selecting
CC siRNA for generating a gene silencing reagent. The present sequence is
CC used in the exemplification of the invention.
XX
SQ Sequence 19 BP; 7 A; 3 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.8%; Score 19; DB 12; Length 19;
Best Local Similarity 73.7%; Pred. No. 9e+05;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 2227 TCACGAAGACAGAGTTATT 2245
:|||||||||||||::|::
Db 1 UCACGAAGACAGAGUUAUU 19

RESULT 44
ADQ62135
ID ADQ62135 standard; RNA; 19 BP.
XX
AC ADQ62135;
XX
DT 09-SEP-2004 (first entry)
XX
DE Anti-TRAF2 siRNA SEQ ID NO:1837.
XX
KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW RNA interference.
XX
OS Synthetic.
XX
PN WO2004045543-A2.
XX
PD 03-JUN-2004.
XX
PF 14-NOV-2003; 2003WO-US036787.
XX
PR 14-NOV-2002; 2002US-0426137P.
PR 10-SEP-2003; 2003US-0502050P.
XX
PA (DHAR-) DHARMACON INC.
XX
PI Anastasia K, Angela R, Devin L, William M, Stephen S;
XX
DR WPI; 2004-420527/39.
XX
PT Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
PT by selecting a target gene and measuring the functionality of the
PT nucleotide sequences that are complementary to a stretch of nucleotides
PT of the target sequence.
XX
PS Example 12; SEQ ID NO 1837; 199pp; English.
XX
CC The invention relates to a novel method for selecting siRNA (short
CC interfering RNA) comprising selecting an siRNA molecule of 19-25
CC nucleoside bases by selecting a target gene and measuring the
CC functionality of sequences of 19-25 nucleotides in length that are
CC substantially complementary to a stretch of nucleotides of the target
CC sequence, where the functionality is dependent upon non-target specific
CC criteria. Also claimed are methods for gene-silencing, developing an
CC siRNA algorithm for selecting siRNA, selecting an siRNA with improved
CC functionality, selecting hyperfunctional siRNA, an siRNA molecule
CC effective at silencing Bcl-2, and a kit for gene silencing comprising the
CC siRNA. The siRNA molecule comprises a sequence substantially similar to a
CC sequence consisting of GGGAGAUAGUGAUGAAGUA; GAAGUACAUCCAUUAUAAG;
CC GUACGACAACCGGGAGAUA; AGAUAGUGAUGAAGUACAU; UGAAGACUCUGCUCAGUUU;
CC CAUGCGGCCUCUGUUUGA; UGCGGCCUCUGUUUGAUUU; GAGAUAGUGAUGAAGUACA;
CC GGAGAUAGUGAUGAAGUAC; and GAAGACUCUGCUCAGUUUG. The siRNA molecule
CC comprises a sense strand and an anti-sense strand. The siRNA molecule
CC comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
CC pairs. The kit comprises at least two siRNA, comprising a first optimised
CC siRNA and a second optimised siRNA. The method is useful in selecting
CC siRNA for generating a gene silencing reagent. The present sequence is
CC used in the exemplification of the invention.
XX
SQ Sequence 19 BP; 8 A; 3 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 0.8%; Score 19; DB 12; Length 19;
Best Local Similarity 78.9%; Pred. No. 9e+05;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2228 CACGAAGACAGAGTTATTA 2246
|||||||||||||::|::|
Db 1 CACGAAGACAGAGUUAUUA 19

RESULT 45
ADQ62134
ID ADQ62134 standard; RNA; 19 BP.
XX
AC ADQ62134;
XX
DT 09-SEP-2004 (first entry)
XX

```
DE   Anti-TRAF2 siRNA SEQ ID NO:1836.
XX
KW   ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW   RNA interference.
XX
OS   Synthetic.
XX
PN   WO2004045543-A2.
XX
PD   03-JUN-2004.
XX
PF   14-NOV-2003; 2003WO-US036787.
XX
PR   14-NOV-2002; 2002US-0426137P.
PR   10-SEP-2003; 2003US-0502050P.
XX
PA   (DHAR-) DHARMACON INC.
XX
PI   Anastasia K,  Angela R,  Devin L,  William M,  Stephen S;
XX
DR   WPI; 2004-420527/39.
XX
PT   Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
PT   by selecting a target gene and measuring the functionality of the
PT   nucleotide sequences that are complementary to a stretch of nucleotides
PT   of the target sequence.
XX
PS   Example 12; SEQ ID NO 1836; 199pp; English.
XX
CC   The invention relates to a novel method for selecting siRNA (short
CC   interfering RNA) comprising selecting an siRNA molecule of 19-25
CC   nucleoside bases by selecting a target gene and measuring the
CC   functionality of sequences of 19-25 nucleotides in length that are
CC   substantially complementary to a stretch of nucleotides of the target
CC   sequence, where the functionality is dependent upon non-target specific
CC   criteria. Also claimed are methods for gene-silencing, developing an
CC   siRNA algorithm for selecting siRNA, selecting an siRNA with improved
CC   functionality, selecting hyperfunctional siRNA, an siRNA molecule
CC   effective at silencing Bcl-2, and a kit for gene silencing comprising the
CC   siRNA. The siRNA molecule comprises a sequence substantially similar to a
CC   sequence consisting of GGGAGAUAGUGAUGAAGUA; GAAGUACAUCCAUUAUAAG;
CC   GUACGACAACCGGGAGAUA; AGAUAGUGAUGAAGUACAU; UGAAGACUCUGCUCAGUUU;
CC   CAUGCGGCCUCUGUUUGA; UGCGGCCUCUGUUUGAUUU; GAGAUAGUGAUGAAGUACA;
CC   GGAGAUAGUGAUGAAGUAC; and GAAGACUCUGCUCAGUUUG. The siRNA molecule
CC   comprises a sense strand and an anti-sense strand. The siRNA molecule
CC   comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
CC   pairs. The kit comprises at least two siRNA, comprising a first optimised
CC   siRNA and a second optimised siRNA. The method is useful in selecting
CC   siRNA for generating a gene silencing reagent. The present sequence is
CC   used in the exemplification of the invention.
XX
SQ   Sequence 19 BP; 9 A; 3 C; 3 G; 0 T; 4 U; 0 Other;

  Query Match             0.8%;  Score 19;  DB 12;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 9e+05;
  Matches   15;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2233 AGACAGAGTTATTAAACCA 2251
              |||||||||::|::||||||
Db          1 AGACAGAGUUAUUAAACCA 19


RESULT 46
AAZ89685/c
ID   AAZ89685 standard; DNA; 30 BP.
XX
AC   AAZ89685;
XX
DT   28-JUN-2000  (first entry)
XX
DE   Human ADAM DNA PCR primer #10.
XX
KW   ADAM protein; human; A disintegrin and metalloprotease; diagnosis;
KW   drug development; intervertebral hernia; sciatica; pulmonary fibrosis;
KW   diabetic nephropathy; hepatic fibrosis; glomerulitis; osteopetrosis;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200014227-A1.
XX
PD   16-MAR-2000.
XX
PF   02-SEP-1999;   99WO-JP004766.
XX
PR   03-SEP-1998;   98JP-00250115.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Yoshimura K,  Hikichi Y,  Nishimura A;
XX
DR   WPI; 2000-271056/23.
XX
PT   Novel protein belong to A disintegrin and metalloprotease family, with
PT   protease activity and extracellular matrix digesting enzyme activity, for
PT   gene diagnosis and developing drugs for treating e.g. sciatica and
PT   glomerulitis.
XX
PS   Example 2; Page 104; 109pp; Japanese.
XX
CC   This invention describes a novel human protein (I) which belongs to the
CC   ADAM (A disintegrin and metalloprotease) protein family. The protein,
CC   peptide fragment and antibody are useful for gene diagnosis and in the
CC   development of drugs to prevent or treat intervertebral hernia, sciatica,
CC   glomerulitis, diabetic nephropathy, hepatic fibrosis, pulmonary fibrosis
CC   or osteopetrosis. AAZ89675-Z89682 represent PCR primer used to amplify
CC   the human ADAM protein which is described in the method of the invention
XX
SQ   Sequence 30 BP; 8 A; 7 C; 7 G; 8 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 19;  DB 3;  Length 30;
  Best Local Similarity   81.5%;  Pred. No. 1e+06;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        703 AGATTCCACGCCATCGGCTGCCTCGAG 729
              |||||||| | ||  |||| ||||||||
Db         27 AGATTCCAAGTCAATGGCTTCCTCGAG 1


RESULT 47
AAT66316
ID   AAT66316 standard; DNA; 30 BP.
XX
AC   AAT66316;
XX
DT   13-MAR-1998  (first entry)
XX
DE   Oligonucleotide from clone 10 from cell intrusion experiment.
XX
KW   Fusion protein; surface; bacterial cell; peptide library; aggregate;
KW   screening; diagnosis; treatment; autoimmune disease; cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9706264-A1.
XX
PD   20-FEB-1997.
XX
PF   05-AUG-1996;   96WO-JP002196.
XX
PR   04-AUG-1995;   95JP-00199745.
XX
PA   (SUME ) SUMITOMO ELECTRIC IND CO.
XX
PI   Shimbara N,  Saya H;
XX
```

DR WPI; 1997-154269/14.
DR P-PSDB; AAW00940.
XX
PT Bacterial peptide library expressing cell invasive protein on the cell
PT surface - bonded to a random target protein which is thus introduced to
PT target cells.
XX
PS Disclosure; Page 45; 86pp; Japanese.
XX
CC Escherichia coli was introduced into VA13 to obtain a cell intrusion E.
CC coli. This was carried out using ESPEL. 22 clones were selected from this
CC and plasmid extracted. DNA sequencing was carried out by Taq cycle
CC sequencing. The invention concerns a fusion protein which presents at the
CC surface of bacterial cells transformed with DNA coding for the fusion
CC protein. Bacterium exhibiting the fused protein on its surface are used
CC to produce a bacterial peptide library which is an aggregate of such
CC bacteria. The bacterial peptide library is useful in identification of
CC target proteins having a desired biochemical activity in target cells,
CC for diagnosis or treatment of diseases such as autoimmune diseases and
CC cancer. The bacterial library readily reproduces and is relatively
CC stable, without significant change or denaturation during preservation
XX
SQ Sequence 30 BP; 7 A; 2 C; 19 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 18.8; DB 2; Length 30;
Best Local Similarity 76.7%; Pred. No. 1.1e+06;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 742 GAGAAACAGCAGGAGCACGAGGTGCAGTGG 771
|||| | | ||||| | |||||||||| ||
Db 1 GAGAGGCGGGAGGAGGATGAGGTGCAGGGG 30

RESULT 48
ABK50863/c
ID ABK50863 standard; DNA; 29 BP.
XX
AC ABK50863;
XX
DT 30-JUL-2002 (first entry)
XX
DE Cholera toxin A sub-unit (CtxA1), reverse PCR primer.
XX
KW Co-expression DNA vaccine; antibacterial; antiviral; antiparasitic;
KW immunostimulant; vaccine; immune response; systemic tolerance;
KW Tat-mediated immune deviation; PCR; primer; ss.
XX
OS Vibrio cholerae.
XX
PN WO200219968-A2.
XX
PD 14-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028365.
XX
PR 08-SEP-2000; 2000US-0231070P.
PR 08-SEP-2000; 2000US-0231376P.
PR 08-SEP-2000; 2000US-0231403P.
PR 08-SEP-2000; 2000US-0231449P.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI Hone D, Lewis G, Fouts T, Bagley K, Boyson M, Obriecht C;
PI Shata M, Agwale S;
XX
DR WPI; 2002-383031/41.
XX
PT Co-expression DNA vaccines comprising an antigen-encoding region and a
PT biologically active component-encoding region, useful as vaccines against
PT viral, bacterial and parasitic pathogens, or for enhancing immune
PT responses.
XX
PS Example 6; Page 51; 108pp; English.
XX
CC The invention describes a new DNA vaccine comprising a region encoding an
CC antigen component and a region encoding at least one biologically active
CC component such as adjuvants, immunoregulatory peptides and proteins,
CC antisense RNAs, and catalytic RNAs. The co-expression DNA vaccines are
CC useful for vaccinating animals against viral, bacterial and parasitic
CC pathogens, for enhancing immune responses, for inducing systemic
CC tolerance, and for treating and/or preventing Tat-mediated immune
CC deviation. The co-expression DNA vaccines are capable of inducing
CC significantly stronger immune responses against vaccine antigens than
CC conventional DNA vaccines, and are also capable of inducing systemic
CC tolerance. This sequence represents a PCR primer used to isolate DNA
CC encoding the cholera toxin sub-unit A (CtxA1), an immunoregulatory
CC molecule useful in the co-expression DNA vaccines described in the
CC invention
XX
SQ Sequence 29 BP; 4 A; 7 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 0.8%; Score 18.6; DB 6; Length 29;
Best Local Similarity 84.0%; Pred. No. 1.2e+06;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1440 CATGAACATCGCAAGCGGCTGCCCC 1464
|| || ||||| ||||||| |||||
Db 25 CAAGATCATCGTAAGCGGCCGCCCC 1

RESULT 49
ABK70442
ID ABK70442 standard; DNA; 30 BP.
XX
AC ABK70442;
XX
DT 15-JUL-2002 (first entry)
XX
DE In-situ analysis synthetic probe #10.
XX
KW Human; oligonucleotide label-domain; CMV; cytomegalovirus; EBV;
KW Epstein-Barr virus; lambda-immunoglobulin light chain; hapten;
KW kappa-immunoglobulin light chain; repetitive Alu sequence; EBER;
KW Epstein-Barr early RNA; probe; ss.
XX
OS Synthetic.
XX
PN WO200222874-A2.
XX
PD 21-MAR-2002.
XX
PF 06-SEP-2001; 2001WO-US028014.
XX
PR 15-SEP-2000; 2000US-0233177P.
XX
PA (VENT-) VENTANA MEDICAL SYSTEMS INC.
XX
PI Utermohlen JG, Connaughton J;
XX
DR WPI; 2002-371972/40.
XX
PT Novel oligonucleotide label-domain for incorporation into oligonucleotide
PT probes useful for detecting or localizing nucleic acid target genes
PT within a cell or tissue sample.
XX
PS Disclosure; Page 59; 71pp; English.
XX
CC The present invention relates to a new oligonucleotide label-domain
CC comprising the sequence (CTATTTT)_n and its complement (AAAATAG)_n, where
CC n is 1. The probe sets of the invention are useful for detecting kappa or
CC lambda-immunoglobulin light chain mRNA or corresponding heteronuclear
CC RNA, CMV (cytomegalovirus) immediate early RNA, EBV (Epstein-Barr virus)
CC early RNA 1 and RNA 2, and human Alu repetitive satellite genomic
CC sequences. The invention is a useful generic sequence for incorporation
CC into oligonucleotide probes for detecting gene-specific sequences within
CC cells or tissue samples in in situ hybridisation analysis and for

CC attaching a label to immunoglobulins or other proteins for detecting
CC haptens and antigens in immunohistochemical analyses. The present nucleic
CC acid sequence represents one of a collection (ABK70376-ABK70501) of
CC oligonucleotide probes that were used in the invention for detecting or
CC localising a plurality nucleic acid target gene or antigen within a cell
CC or tissue sample
XX
SQ Sequence 30 BP; 1 A; 8 C; 9 G; 12 T; 0 U; 0 Other;

Query Match 0.8%; Score 18.6; DB 6; Length 30;
Best Local Similarity 84.0%; Pred. No. 1.3e+06;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1836 GCTGCCCTTGCTGTCCTGTGCAGTG 1860
|||| ||||||||||||| | |||
Db 6 GCTGTCCTTGCTGTCCTGCTCTGTG 30

RESULT 50
ACI67643
ID ACI67643 standard; DNA; 25 BP.
XX
AC ACI67643;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 67634.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 67634; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ Sequence 25 BP; 5 A; 9 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 18.4; DB 9; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.3e+06;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 747 ACAGCAGGAGCACGAGGTGC 766
|||||||||||||| |||||
Db 5 ACAGCAGGAGCACGCGGTGC 24

Search completed: November 20, 2004, 04:40:54
Job time : 1078 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 19, 2004, 17:55:50 ; Search time 9562 Seconds
(without alignments)
11186.917 Million cell updates/sec

Title: US-10-067-125-2
Perfect score: 2262
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1393428

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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2: gb_htg:*
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5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	24	1.1	24	6	AX937536	AX937536 Sequence
	2	23	1.0	23	6	CQ799591	CQ799591 Sequence
c	3	23	1.0	23	6	CQ799592	CQ799592 Sequence
	4	23	1.0	30	6	A66652	A66652 Sequence 8
	5	23	1.0	30	6	AX089601	AX089601 Sequence
	6	22	1.0	22	6	AX937535	AX937535 Sequence
	7	20.6	0.9	21	6	AX096586	AX096586 Sequence
	8	20.6	0.9	21	6	AX154242	AX154242 Sequence
c	9	20	0.9	20	6	BD224912	BD224912 Antisense
c	10	20	0.9	20	6	BD224913	BD224913 Antisense
c	11	20	0.9	20	6	BD224914	BD224914 Antisense
c	12	20	0.9	20	6	BD224915	BD224915 Antisense
c	13	20	0.9	20	6	BD224916	BD224916 Antisense
c	14	20	0.9	20	6	BD224917	BD224917 Antisense
c	15	20	0.9	20	6	BD224918	BD224918 Antisense
c	16	20	0.9	20	6	BD224919	BD224919 Antisense
c	17	20	0.9	20	6	BD224920	BD224920 Antisense
c	18	20	0.9	20	6	BD224921	BD224921 Antisense
c	19	20	0.9	20	6	BD224922	BD224922 Antisense
c	20	20	0.9	20	6	BD224923	BD224923 Antisense
c	21	20	0.9	20	6	BD224924	BD224924 Antisense
c	22	20	0.9	20	6	BD224925	BD224925 Antisense
c	23	20	0.9	20	6	BD224926	BD224926 Antisense
c	24	20	0.9	20	6	BD224927	BD224927 Antisense
c	25	20	0.9	20	6	BD224928	BD224928 Antisense
c	26	20	0.9	20	6	BD224929	BD224929 Antisense
c	27	20	0.9	20	6	BD224930	BD224930 Antisense
c	28	20	0.9	20	6	BD224931	BD224931 Antisense
c	29	20	0.9	20	6	BD224932	BD224932 Antisense
c	30	20	0.9	20	6	BD224933	BD224933 Antisense
c	31	20	0.9	20	6	AR211134	AR211134 Sequence
c	32	20	0.9	20	6	AR211135	AR211135 Sequence
c	33	20	0.9	20	6	AR211136	AR211136 Sequence
c	34	20	0.9	20	6	AR211137	AR211137 Sequence
c	35	20	0.9	20	6	AR211138	AR211138 Sequence
c	36	20	0.9	20	6	AR211139	AR211139 Sequence
c	37	20	0.9	20	6	AR211140	AR211140 Sequence
c	38	20	0.9	20	6	AR211141	AR211141 Sequence
c	39	20	0.9	20	6	AR211142	AR211142 Sequence
c	40	20	0.9	20	6	AR211143	AR211143 Sequence
c	41	20	0.9	20	6	AR211144	AR211144 Sequence
c	42	20	0.9	20	6	AR211145	AR211145 Sequence
c	43	20	0.9	20	6	AR211146	AR211146 Sequence
c	44	20	0.9	20	6	AR211147	AR211147 Sequence
c	45	20	0.9	20	6	AR211148	AR211148 Sequence
c	46	20	0.9	20	6	AR211149	AR211149 Sequence
c	47	20	0.9	20	6	AR211150	AR211150 Sequence
c	48	20	0.9	20	6	AR211151	AR211151 Sequence
c	49	20	0.9	20	6	AR211152	AR211152 Sequence
c	50	20	0.9	20	6	AR211153	AR211153 Sequence

ALIGNMENTS

RESULT 1
AX937536/c
LOCUS AX937536 24 bp DNA linear PAT 06-JAN-2004
DEFINITION Sequence 16 from Patent EP1361433.
ACCESSION AX937536
VERSION AX937536.1 GI:40713576
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Yanai,Y.C., Yamamoto,S.C., Yamamoto,K.C. and Ikegami,H.C.
TITLE Method for estimating therapeutic efficacy of tumor necrosis factor (TNF)
JOURNAL Patent: EP 1361433-A 16 12-NOV-2003;
KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO (JP)
FEATURES Location/Qualifiers
source 1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide used as primer for PCR detection of TRAF2 mRNA"
ORIGIN

Query Match 1.1%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1223 TGTGTCTGCGTATCTACCTGAACG 1246
||||||||||||||||||||||||
Db 24 TGTGTCTGCGTATCTACCTGAACG 1

RESULT 2
CQ799591
LOCUS CQ799591 23 bp DNA linear PAT 28-APR-2004

```
DEFINITION  Sequence 241 from Patent WO2004031413.
ACCESSION   CQ799591
VERSION     CQ799591.1  GI:46848538
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Nakamura,Y., Daigo,Y. and Nakatsuru,S.
  TITLE     Method for diagnosing non-small cell lung cancers
  JOURNAL   Patent: WO 2004031413-A 241 15-APR-2004;
            Oncotherapy Science, Inc. (JP); Japan as represented by the
            president of the university of Tokyo (JP)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Artificially synthesized primer sequence for
                     RT-PCR"
ORIGIN

  Query Match             1.0%;  Score 23;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+06;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1224 GTGTCTGCGTATCTACCTGAACG 1246
              |||||||||||||||||||||||
Db          1 GTGTCTGCGTATCTACCTGAACG 23


RESULT 3
CQ799592/c
LOCUS       CQ799592                  23 bp    DNA     linear   PAT 28-APR-2004
DEFINITION  Sequence 242 from Patent WO2004031413.
ACCESSION   CQ799592
VERSION     CQ799592.1  GI:46848539
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Nakamura,Y., Daigo,Y. and Nakatsuru,S.
  TITLE     Method for diagnosing non-small cell lung cancers
  JOURNAL   Patent: WO 2004031413-A 242 15-APR-2004;
            Oncotherapy Science, Inc. (JP); Japan as represented by the
            president of the university of Tokyo (JP)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
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                     RT-PCR"
ORIGIN

  Query Match             1.0%;  Score 23;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+06;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2222 CCAGCTCACGAAGACAGAGTTAT 2244
              |||||||||||||||||||||||
Db         23 CCAGCTCACGAAGACAGAGTTAT 1


RESULT 4
A66652
LOCUS       A66652                    30 bp    DNA     linear   PAT 29-MAR-1999
DEFINITION  Sequence 8 from Patent WO9737016.
ACCESSION   A66652
VERSION     A66652.1  GI:4538142
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Wallach,D., Malinin,N., Boldin,M., Kovalenko,A. and Mett,I.
  TITLE     MODULATORS OF TNF RECEPTOR ASSOCIATED FACTOR (TRAF), THEIR
            PREPARATION AND USE
  JOURNAL   Patent: WO 9737016-A 8 09-OCT-1997;
            YEDA RES & DEV (IL)
COMMENT     Other publication AU 2175597 19971022.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             1.0%;  Score 23;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+06;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 CTCATGGCTGCAGCTAGCGTGAC 74
              |||||||||||||||||||||||
Db          8 CTCATGGCTGCAGCTAGCGTGAC 30


RESULT 5
AX089601
LOCUS       AX089601                  30 bp    DNA     linear   PAT 21-MAR-2001
DEFINITION  Sequence 1 from Patent WO0116314.
ACCESSION   AX089601
VERSION     AX089601.1  GI:13443793
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wallach,D., Malinin,N., Sinha,I.W. and Leu,S.
  TITLE     Iren protein, its preparation and use
  JOURNAL   Patent: WO 0116314-A 1 08-MAR-2001;
            YEDA RESEARCH AND DEVELOPMENT Co. LTD. (IL)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA Sequence"
ORIGIN

  Query Match             1.0%;  Score 23;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+06;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 CTCATGGCTGCAGCTAGCGTGAC 74
              |||||||||||||||||||||||
Db          8 CTCATGGCTGCAGCTAGCGTGAC 30


RESULT 6
AX937535
LOCUS       AX937535                  22 bp    DNA     linear   PAT 06-JAN-2004
DEFINITION  Sequence 15 from Patent EP1361433.
ACCESSION   AX937535
VERSION     AX937535.1  GI:40713575
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Yanai,Y.C., Yamamoto,S.C., Yamamoto,K.C. and Ikegami,H.C.
  TITLE     Method for estimating therapeutic efficacy of tumor necrosis factor
            (TNF)
  JOURNAL   Patent: EP 1361433-A 15 12-NOV-2003;
            KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO (JP)
```

```
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide used as primer for PCR detection of
                     TRAF2 mRNA"
ORIGIN

  Query Match             1.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+06;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        904 AACATTGTCTGCGTCCTGAACC 925
              ||||||||||||||||||||||
Db          1 AACATTGTCTGCGTCCTGAACC 22


RESULT 7
AX096586
LOCUS       AX096586                  21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 1764 from Patent WO0118250.
ACCESSION   AX096586
VERSION     AX096586.1  GI:13512840
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 1764 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             0.9%;  Score 20.6;  DB 6;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 1.1e+07;
  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        434 GCCGCTGCCCGCTCATGCTGA 454
              ||||||||||:||||||||||
Db          1 GCCGCTGCCCRCTCATGCTGA 21


RESULT 8
AX154242
LOCUS       AX154242                  21 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 340 from Patent WO0138576.
ACCESSION   AX154242
VERSION     AX154242.1  GI:14535856
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE     Human single nucleotide polymorphisms
  JOURNAL   Patent: WO 0138576-A 340 31-MAY-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             0.9%;  Score 20.6;  DB 6;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 1.1e+07;
  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        701 GCAGATTCCACGCCATCGGCT 721
              ||||||||||:||||||||||
Db          1 GCAGATTCCASGCCATCGGCT 21


RESULT 9
BD224912/c
LOCUS       BD224912                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224912
VERSION     BD224912.1  GI:33034682
KEYWORDS    JP 2002526095-A/47.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 47 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/47
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCCGGCGCGCTGCGAC 20
              ||||||||||||||||||||
Db         20 GAATTCCGGCGCGCTGCGAC 1


RESULT 10
BD224913/c
LOCUS       BD224913                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224913
VERSION     BD224913.1  GI:33034683
KEYWORDS    JP 2002526095-A/48.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 48 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
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            PN   JP 2002526095-A/48
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CGGCGCGCTGCGACCGTTGG 26
              ||||||||||||||||||||
Db         20 CGGCGCGCTGCGACCGTTGG 1


RESULT 11
BD224914/c
LOCUS       BD224914                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224914
VERSION     BD224914.1  GI:33034684
KEYWORDS    JP 2002526095-A/49.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 49 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/49
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 GGTCACAGCTCTCATGGCTG 61
              ||||||||||||||||||||
Db         20 GGTCACAGCTCTCATGGCTG 1


RESULT 12
BD224915/c
LOCUS       BD224915                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224915
VERSION     BD224915.1  GI:33034685
KEYWORDS    JP 2002526095-A/50.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 50 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/50
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 CTCATGGCTGCAGCTAGCGT 71
              ||||||||||||||||||||
Db         20 CTCATGGCTGCAGCTAGCGT 1


RESULT 13
BD224916/c
LOCUS       BD224916                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224916
VERSION     BD224916.1  GI:33034686
KEYWORDS    JP 2002526095-A/51.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 51 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/51
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
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                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        185 CCTTCCAGGCGCAGTGTGGC 204
              ||||||||||||||||||||
Db         20 CCTTCCAGGCGCAGTGTGGC 1


RESULT 14
BD224917/c
LOCUS       BD224917                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224917
VERSION     BD224917.1  GI:33034687
KEYWORDS    JP 2002526095-A/52.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 52 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/52
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
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                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        348 GGAGGTGGAGAGCCTGCCGG 367
              ||||||||||||||||||||
Db         20 GGAGGTGGAGAGCCTGCCGG 1


RESULT 15
BD224918/c
LOCUS       BD224918                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224918
VERSION     BD224918.1  GI:33034688
KEYWORDS    JP 2002526095-A/53.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 53 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/53
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        422 GCTGCCACGAAGGCCGCTGC 441
              ||||||||||||||||||||
Db         20 GCTGCCACGAAGGCCGCTGC 1


RESULT 16
BD224919/c
LOCUS       BD224919                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224919
VERSION     BD224919.1  GI:33034689
KEYWORDS    JP 2002526095-A/54.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 54 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/54
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        576 CGTGAAGGCGCACCACGAGG 595
              ||||||||||||||||||||
Db         20 CGTGAAGGCGCACCACGAGG 1


RESULT 17
BD224920/c
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LOCUS       BD224920                20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224920
VERSION     BD224920.1  GI:33034690
KEYWORDS    JP 2002526095-A/55.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 55 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/55
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        675 GACTTGTGGCAAGTGTCGAG 694
              ||||||||||||||||||||
Db         20 GACTTGTGGCAAGTGTCGAG 1


RESULT 18
BD224921/c
LOCUS       BD224921                20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224921
VERSION     BD224921.1  GI:33034691
KEYWORDS    JP 2002526095-A/56.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 56 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/56
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        751 CAGGAGCACGAGGTGCAGTG 770
              ||||||||||||||||||||
Db         20 CAGGAGCACGAGGTGCAGTG 1


RESULT 19
BD224922/c
LOCUS       BD224922                20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224922
VERSION     BD224922.1  GI:33034692
KEYWORDS    JP 2002526095-A/57.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 57 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/57
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        848 GGTCAGAGCTCCTGCAGAGG 867
              ||||||||||||||||||||
Db         20 GGTCAGAGCTCCTGCAGAGG 1


RESULT 20
BD224923/c
LOCUS       BD224923                20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224923
VERSION     BD224923.1  GI:33034693
KEYWORDS    JP 2002526095-A/58.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 58 20-AUG-2002;
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            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/58
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        962 GCAGCCGGCAGCACCGGCTG 981
              ||||||||||||||||||||
Db         20 GCAGCCGGCAGCACCGGCTG 1


RESULT 21
BD224924/c
LOCUS       BD224924                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224924
VERSION     BD224924.1  GI:33034694
KEYWORDS    JP 2002526095-A/59.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 59 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/59
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1240 CTGAACGGCGACGGCACCGG 1259
              ||||||||||||||||||||
Db         20 CTGAACGGCGACGGCACCGG 1


RESULT 22
BD224925/c
LOCUS       BD224925                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224925
VERSION     BD224925.1  GI:33034695
KEYWORDS    JP 2002526095-A/60.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 60 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/60
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1387 GACGCCTTCAGGCCCGACGT 1406
              ||||||||||||||||||||
Db         20 GACGCCTTCAGGCCCGACGT 1


RESULT 23
BD224926/c
LOCUS       BD224926                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224926
VERSION     BD224926.1  GI:33034696
KEYWORDS    JP 2002526095-A/61.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 61 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/61
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1533 GGCCATTGTGGACCTGACAG 1552
              ||||||||||||||||||||
Db         20 GGCCATTGTGGACCTGACAG 1


RESULT 24
BD224927/c
LOCUS       BD224927                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224927
VERSION     BD224927.1  GI:33034697
KEYWORDS    JP 2002526095-A/62.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 62 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/62
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1590 GGCAGCCAGGCACAGCCGGC 1609
              ||||||||||||||||||||
Db         20 GGCAGCCAGGCACAGCCGGC 1


RESULT 25
BD224928/c
LOCUS       BD224928                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224928
VERSION     BD224928.1  GI:33034698
KEYWORDS    JP 2002526095-A/63.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 63 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/63
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1685 GGTGTCGGCCTGCAGCCAAG 1704
              ||||||||||||||||||||
Db         20 GGTGTCGGCCTGCAGCCAAG 1


RESULT 26
BD224929/c
LOCUS       BD224929                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224929
VERSION     BD224929.1  GI:33034699
KEYWORDS    JP 2002526095-A/64.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 64 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/64
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1789 GGCTGTGGTGGCATTGGCCG 1808
              ||||||||||||||||||||
Db         20 GGCTGTGGTGGCATTGGCCG 1
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RESULT 27
BD224930/c
LOCUS       BD224930                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224930
VERSION     BD224930.1  GI:33034700
KEYWORDS    JP 2002526095-A/65.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 65 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/65
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1916 CCATGTAGCAGGAGCACAGT 1935
              ||||||||||||||||||||
Db         20 CCATGTAGCAGGAGCACAGT 1


RESULT 28
BD224931/c
LOCUS       BD224931                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224931
VERSION     BD224931.1  GI:33034701
KEYWORDS    JP 2002526095-A/66.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 66 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/66
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1994 GGCCTCCTGCTGGCCAGAGC 2013
              ||||||||||||||||||||
Db         20 GGCCTCCTGCTGGCCAGAGC 1


RESULT 29
BD224932/c
LOCUS       BD224932                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224932
VERSION     BD224932.1  GI:33034702
KEYWORDS    JP 2002526095-A/67.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 67 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/67
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2117 CTTGGCCAGGCTGGCTGTGG 2136
              ||||||||||||||||||||
Db         20 CTTGGCCAGGCTGGCTGTGG 1


RESULT 30
BD224933/c
LOCUS       BD224933                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Antisense modulation of expression of tumor necrosis factor
            receptor-associated factor (TRAF).
ACCESSION   BD224933
VERSION     BD224933.1  GI:33034703
KEYWORDS    JP 2002526095-A/68.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
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            receptor-associated factor (TRAF)
  JOURNAL   Patent: JP 2002526095-A 68 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526095-A/68
            PD   20-AUG-2002
            PF   05-OCT-1999 JP 2000574546
            PR   06-OCT-1998 US    09/167109
            PI   BRENDA F BAKER,LEX M COWSERT,BRETT P MONIA,XIAOXING S XU PC
            C12N15/09,A61K31/7105,A61K48/00,A61P29/00,A61P35/04,C12N15/00 CC
            antisense sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2221 TCCAGCTCACGAAGACAGAG 2240
              ||||||||||||||||||||
Db         20 TCCAGCTCACGAAGACAGAG 1


RESULT 31
AR211134/c
LOCUS       AR211134                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 47 from patent US 6399297.
ACCESSION   AR211134
VERSION     AR211134.1  GI:21514376
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 47 04-JUN-2002;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCCGGCGCGCTGCGAC 20
              ||||||||||||||||||||
Db         20 GAATTCCGGCGCGCTGCGAC 1


RESULT 32
AR211135/c
LOCUS       AR211135                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 48 from patent US 6399297.
ACCESSION   AR211135
VERSION     AR211135.1  GI:21514377
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 48 04-JUN-2002;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CGGCGCGCTGCGACCGTTGG 26
              ||||||||||||||||||||
Db         20 CGGCGCGCTGCGACCGTTGG 1


RESULT 33
AR211136/c
LOCUS       AR211136                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 49 from patent US 6399297.
ACCESSION   AR211136
VERSION     AR211136.1  GI:21514379
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 49 04-JUN-2002;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 GGTCACAGCTCTCATGGCTG 61
              ||||||||||||||||||||
Db         20 GGTCACAGCTCTCATGGCTG 1


RESULT 34
AR211137/c
LOCUS       AR211137                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 50 from patent US 6399297.
ACCESSION   AR211137
VERSION     AR211137.1  GI:21514380
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 50 04-JUN-2002;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 CTCATGGCTGCAGCTAGCGT 71
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              ||||||||||||||||||||
Db         20 CTCATGGCTGCAGCTAGCGT 1


RESULT 35
AR211138/c
LOCUS       AR211138                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 51 from patent US 6399297.
ACCESSION   AR211138
VERSION     AR211138.1  GI:21514381
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 51 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        185 CCTTCCAGGCGCAGTGTGGC 204
              ||||||||||||||||||||
Db         20 CCTTCCAGGCGCAGTGTGGC 1


RESULT 36
AR211139/c
LOCUS       AR211139                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 52 from patent US 6399297.
ACCESSION   AR211139
VERSION     AR211139.1  GI:21514382
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 52 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        348 GGAGGTGGAGAGCCTGCCGG 367
              ||||||||||||||||||||
Db         20 GGAGGTGGAGAGCCTGCCGG 1


RESULT 37
AR211140/c
LOCUS       AR211140                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 53 from patent US 6399297.
ACCESSION   AR211140
VERSION     AR211140.1  GI:21514384
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 53 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        422 GCTGCCACGAAGGCCGCTGC 441
              ||||||||||||||||||||
Db         20 GCTGCCACGAAGGCCGCTGC 1


RESULT 38
AR211141/c
LOCUS       AR211141                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 54 from patent US 6399297.
ACCESSION   AR211141
VERSION     AR211141.1  GI:21514385
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 54 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        576 CGTGAAGGCGCACCACGAGG 595
              ||||||||||||||||||||
Db         20 CGTGAAGGCGCACCACGAGG 1


RESULT 39
AR211142/c
LOCUS       AR211142                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 55 from patent US 6399297.
ACCESSION   AR211142
VERSION     AR211142.1  GI:21514386
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 55 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
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  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        675 GACTTGTGGCAAGTGTCGAG 694
              ||||||||||||||||||||
Db         20 GACTTGTGGCAAGTGTCGAG 1


RESULT 40
AR211143/c
LOCUS       AR211143                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 56 from patent US 6399297.
ACCESSION   AR211143
VERSION     AR211143.1  GI:21514387
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 56 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        751 CAGGAGCACGAGGTGCAGTG 770
              ||||||||||||||||||||
Db         20 CAGGAGCACGAGGTGCAGTG 1


RESULT 41
AR211144/c
LOCUS       AR211144                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 57 from patent US 6399297.
ACCESSION   AR211144
VERSION     AR211144.1  GI:21514389
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 57 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        848 GGTCAGAGCTCCTGCAGAGG 867
              ||||||||||||||||||||
Db         20 GGTCAGAGCTCCTGCAGAGG 1


RESULT 42
AR211145/c
LOCUS       AR211145                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 58 from patent US 6399297.
ACCESSION   AR211145
VERSION     AR211145.1  GI:21514390
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 58 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        962 GCAGCCGGCAGCACCGGCTG 981
              ||||||||||||||||||||
Db         20 GCAGCCGGCAGCACCGGCTG 1


RESULT 43
AR211146/c
LOCUS       AR211146                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 59 from patent US 6399297.
ACCESSION   AR211146
VERSION     AR211146.1  GI:21514391
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 59 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1240 CTGAACGGCGACGGCACCGG 1259
              ||||||||||||||||||||
Db         20 CTGAACGGCGACGGCACCGG 1


RESULT 44
AR211147/c
LOCUS       AR211147                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 60 from patent US 6399297.
ACCESSION   AR211147
VERSION     AR211147.1  GI:21514393
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 60 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1387 GACGCCTTCAGGCCCGACGT 1406
              ||||||||||||||||||||
Db         20 GACGCCTTCAGGCCCGACGT 1


RESULT 45
AR211148/c
LOCUS       AR211148                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 61 from patent US 6399297.
ACCESSION   AR211148
VERSION     AR211148.1  GI:21514394
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 61 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1533 GGCCATTGTGGACCTGACAG 1552
              ||||||||||||||||||||
Db         20 GGCCATTGTGGACCTGACAG 1


RESULT 46
AR211149/c
LOCUS       AR211149                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 62 from patent US 6399297.
ACCESSION   AR211149
VERSION     AR211149.1  GI:21514395
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 62 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1590 GGCAGCCAGGCACAGCCGGC 1609
              ||||||||||||||||||||
Db         20 GGCAGCCAGGCACAGCCGGC 1


RESULT 47
AR211150/c
LOCUS       AR211150                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 63 from patent US 6399297.
ACCESSION   AR211150
VERSION     AR211150.1  GI:21514396
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 63 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1685 GGTGTCGGCCTGCAGCCAAG 1704
              ||||||||||||||||||||
Db         20 GGTGTCGGCCTGCAGCCAAG 1


RESULT 48
AR211151/c
LOCUS       AR211151                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 64 from patent US 6399297.
ACCESSION   AR211151
VERSION     AR211151.1  GI:21514398
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 64 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1789 GGCTGTGGTGGCATTGGCCG 1808
              ||||||||||||||||||||
Db         20 GGCTGTGGTGGCATTGGCCG 1


RESULT 49
AR211152/c
LOCUS       AR211152                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 65 from patent US 6399297.
ACCESSION   AR211152
VERSION     AR211152.1  GI:21514399
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
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  JOURNAL   Patent: US 6399297-A 65 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1916 CCATGTAGCAGGAGCACAGT 1935
              ||||||||||||||||||||
Db         20 CCATGTAGCAGGAGCACAGT 1


RESULT 50
AR211153/c
LOCUS       AR211153                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 66 from patent US 6399297.
ACCESSION   AR211153
VERSION     AR211153.1  GI:21514400
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Baker,B.F., Cowsert,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
            receptor-associated factors (TRAFs)
  JOURNAL   Patent: US 6399297-A 66 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             0.9%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1994 GGCCTCCTGCTGGCCAGAGC 2013
              ||||||||||||||||||||
Db         20 GGCCTCCTGCTGGCCAGAGC 1


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